

A COMMUNITY APPROACH TO IDENTIFYING ESSENTIAL FISH HABITAT OF  
SPOTTED SEATROUT, *CYNOSCION NEBULOSUS*, IN BARATARIA BAY, LA.

A Dissertation

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## ABSTRACT

Louisiana wetlands are disappearing at a dramatic rate, providing an impetus for identifying essential fish habitat (EFH) in this region. The distribution, relative abundance, biomass, length and food web dynamics of spotted seatrout, *Cynoscion nebulosus*, as well as the fish assemblage structure were examined in Barataria Bay, LA, in relation to habitat type and physical/chemical properties of the water. All fish were collected from three sites located along a salinity gradient, each contained the three habitat types of interest: marsh edge, soft bottom and oyster shell, and were sampled monthly from May 2003 to May 2004 with gillnets. Habitat preference of spotted seatrout was not easily defined by habitat type alone, but rather their distribution, relative abundance, biomass and length distribution were influenced by a combination of habitat and physical/chemical properties of the water. Stable isotope analyses suggest that individual spotted seatrout may not move widely throughout Barataria Bay, but rather they may exhibit some site fidelity with preference for salinity ranges within the bay. Salinity was also an important variable structuring the fish assemblage in Barataria Bay, resulting in a distinct composition of species at the oligohaline site as compared to the mesohaline and polyhaline sites. The fish assemblage structure also differed among habitat types and could generally be divided into three categories; those species only or mostly found at the marsh edge, those species found at all three habitat types, and a few species that had a higher affinity for soft bottom and oyster shell habitats. These results suggest that habitat type and physical/chemical properties of the water work in concert with one another to provide a diverse range of available habitats important to estuarine fishes. Despite the importance of incorporating habitat in fisheries management, it may not be possible to identify which habitats are essential versus which ones are temporarily occupied. This study demonstrates that identifying EFH is a

difficult task and illustrates that an ecosystem approach may be the best method when working towards identifying EFH given the influence of the physical/chemical properties of the water and the species-specific habitat associations identified in this study.

## GENERAL INTRODUCTION

The Sustainable Fisheries Act, an amendment to the Magnuson-Stevens Fishery Conservation and Management Act in 1996, mandated a fishery management approach that focused on the protection and conservation of habitat important to finfish and shellfish. This included a call for the description and identification of essential fish habitat (EFH), defined as ‘those waters and substrate necessary to fish for spawning, breeding, feeding or growth to maturity’, for federally managed fish species (NMFS 1997). This call to attention of the importance of habitat in fishery management has since prompted many fishery managers outside of federal fisheries to identify EFH within their waters.

Identifying the proper tools to measure fish habitat use is one of the first steps in working towards identifying and describing EFH. Traditional active and passive capture techniques used in fisheries have been summarized by Hayes et al. (1996) and Hubert (1996), respectively. These traditional gears are often time and labor intensive and can be biased in many ways (e.g., size, behavior, and saturation) (Hayes et al. 1996; Hubert 1996). Moreover, estimates of species composition and relative abundance from various sampling gears can differ greatly, providing inconsistent and often contradictory results about fish assemblage structure and abundance (Jackson and Harvey 1997). An additional difficulty in choosing an appropriate sampling gear is that certain gear more easily samples some habitats (Hayes et al. 1996; Hubert 1996).

Three habitat types dominate estuaries in Louisiana: marsh, soft bottom (sand /mud) and oyster shell. The value of marshes (Boesch and Turner 1984; Peterson and Turner 1994; Baltz et al. 1993; Stunz et al. 2002) and oyster reef/shell habitat (Zimmerman et al. 1989; Coen et al. 1999) as nursery, feeding and breeding habitat for fishes is well recognized. However, the relative value of these habitats and how they compare to each other, and to soft bottom habitat is

largely unknown. Moreover, habitat specific use has not been documented for many estuarine species (Minello 1999).

In 2001 researchers at Louisiana State University (LSU) came together with the Louisiana Department of Wildlife and Fisheries (LDWF) to identify EFH in coastal Louisiana, specifically focusing on species of recreational importance within the state. The overall goal of the project was to combine what was already known about species composition and relative abundance in Barataria Bay, LA, based on a long-term fisheries monitoring program by LDWF, which is not collected in a habitat specific manner, with new data collected by LSU that focused on sampling in specific habitats with multiple gear types. The first step in this joint venture was to use Klein digital side-scan sonar to differentiate oyster shell bottom from soft bottom (mud/sand) at the sites sampled by both LDWF and LSU in Barataria Bay. The swath format of the side-scan sonar provides a two dimensional acoustic image of bottom hardness (reflectance), surface texture (roughness) and topography. Habitat specific sampling locations within each site were chosen from these side-scan surveys. In addition, SCUBA collections of bottom sediments were made to confirm the bottom-type of habitats.

The steps of the EFH study included: 1) describe fish use of the marsh surface and edge based on catches of various sampling gears (e.g., seine and lift nets) by examining species composition, relative abundance, directional movement, differences between vegetation types and relationships with marsh morphology; 2) estimate size distribution, relative abundance and biomass of the fish assemblage among soft bottom and oyster shell habitats using dual beam hydroacoustic equipment; 3) examine species composition, richness, relative abundance and biomass of fish assemblages associated with marsh edge, soft bottom and oyster shell habitats using gill nets; 4) to use data collected by gill nets to ground truth hydroacoustic data; 5)

determine if there is a link between resource use and habitat utilization of recreationally important species, with gut content and stable isotope analyses; and 6) to compare the composition and relative abundance of fish collected by the LSU gill net soaking method, the LDWF gill net striking method and hydroacoustics.

My role in this project was to work towards the identification and description of EFH of in Barataria Bay, with a special emphasis on spotted seatrout, one of the most highly sought recreational species in coastal Louisiana and to examine resource use of spotted seatrout among habitats and sites with stable isotopes. In Chapter 1 I describe the habitat preferences of spotted seatrout among marsh edge, soft bottom and oyster shell habitats, and in relation to physical/chemical properties of the water. In this chapter I describe the distribution, relative abundance, biomass and length of spotted seatrout. Habitat use was further examined by examining the resource use and the distribution of spotted in Chapter 2 using the composition of  $\delta^{13}\text{C}$ Carbon,  $\delta^{15}\text{N}$ Nitrogen and  $\delta^{34}\text{S}$ Sulfur stable isotopes of spotted seatrout collected from marsh edge, soft bottom and oyster shell habitats at sites located along a salinity gradient in Barataria Bay. The isotopic composition of spotted seatrout tissue and the isotopic composition of the gut contents were compared to determine if there is a match between short-term and long-term foraging of spotted seatrout. Spotted seatrout length and isotopic composition were also examined to describe the relationship between  $\delta^{13}\text{C}$ Carbon,  $\delta^{15}\text{N}$ Nitrogen and  $\delta^{34}\text{S}$ Sulfur and length. I go beyond a single species approach of identifying and describing EFH in Chapter 3 where I examined the habitat use of the Barataria Bay fish assemblage by investigating species composition, richness, relative abundance, and biomass among marsh edge, soft bottom and oyster shell habitats and in relation to the physical/chemical properties of the water.

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# CHAPTER 1: HABITAT PREFERENCES OF SPOTTED SEATROUT, *CYNOSCION NEBULOSUS*, IN BARATARIA BAY, LOUISIANA: A STEP TOWARDS IDENTIFYING ESSENTIAL FISH HABITAT

## **Introduction**

Louisiana wetlands are disappearing at a dramatic rate. While this is true across the nation, with approximately half the nation's original wetland habitats lost over the past 200 years (Dahl et al. 1991), Louisiana currently accounts for about 90% of the total marsh loss in the United States (Dahl 2000; Field et al. 1991). This habitat loss may be detrimental to fishes and macroinvertebrates that rely on salt marshes at some point in their life history (Rakocinski et al. 1992; Baltz et al. 1993; Peterson and Turner 1994). An estimated 97% of commercially harvested fishes in the Louisiana Gulf of Mexico region depend on this and adjacent estuarine basins at some point in their life history (Nelson et al. 2002). This estimate includes approximately 20% of US commercial harvest and about 500 million pounds of fish and shellfish per year (Nelson et al. 2002). Gosselink (1984) suggested that marsh deterioration results from a local imbalance between building processes such as sedimentation, growth of vegetation, accumulation of dead organic matter and destructive processes such as erosion, sea-level rise, crustal subsidence and compaction. In Louisiana there are four major working hypotheses to explain wetland loss: 1) consequences of extensive canal dredging; 2) a decline in suspended sediment load in the Mississippi River; 3) extensive levee construction; and, 4) salt water intrusion (Turner 1997). The area undergoing the greatest wetland loss is in Louisiana is in the Barataria-Terrebonne Estuarine Basin (Barras et al. 1994).

Given the regional focus on marsh habitat loss it is easy to lose sight of the fact that most estuaries have a variety of habitats that exist in a mosaic, providing a complex environment for associated mobile species (Bell et al. 1991). Posey et al. (2000) emphasized that habitat types are

not isolated units, but interconnected and should be managed as such. Despite this, the density of fish often varies among habitat types, and detecting these differences can provide useful information on relative value (Baltz et al. 1993; Minello 1999), habitat selection (Stunz et al. 2001) and differential mortality (Stunz and Minello 2001) associated with these habitat types.

Three habitat types dominate estuaries in Louisiana: marsh, soft bottom (mud/sand) and oyster shell. The value of marshes (Boesch and Turner 1984; Peterson and Turner 1994; Baltz et al. 1993; Stunz et al. 2002) and oyster reef/shell habitat (Zimmerman et al. 1989; Coen et al. 1999) as nursery, feeding and breeding habitat for fish is well recognized. However, the relative value of these habitats and how they compare to each other and to soft bottom habitat is largely unknown. Moreover, habitat specific use has not been documented for many estuarine species (Minello 1999). The majority of scientists that examined habitat selection by fish focused on newly settled larval fish (Boehlert and Mundy 1988, Petrik et al. 1999; Stunz et al. 2002) and juvenile fish (Stunz and Minello 2001). Stunz et al. (2002) incorporated marsh edge, seagrass, soft bottom and oyster reefs into a comparison of habitat use by newly settled larval fish. They found that in areas with no seagrass, density of newly settled red drum, *Sciaenops ocellatus*, was highest at marsh edge habitats compared to non-vegetated habitats and that no settlement was observed over the oyster reef habitat. Stunz and Minello (2001) examined prey vulnerability among marsh edge, oyster reef and non-vegetated bottom and found that juvenile red drum were least vulnerable to predation at the oyster reef habitat followed by marsh edge and non-vegetated habitats. Beyond these studies, most habitat comparisons of fish contrast their use of vegetated vs. non-vegetated areas (Orth et al. 1984; Pollard 1984; Zimmerman et al. 1984; Baltz et al. 1993; Rozas and Zimmerman 2000).

The Sustainable Fisheries Act, a 1996 amendment to the Magnuson-Stevens Fishery Conservation and Management Act, mandated a fishery management approach that focused on the protection and conservation of habitat important to finfish and shellfish. This included a call for the description and identification of essential fish habitat (EFH), defined as ‘those waters and substrate necessary to fish for spawning, breeding, feeding or growth to maturity’, for federally managed fish species (NMFS 1997). The ambiguity of this definition prompted the National Marine Fisheries Service (NMFS) to later define four levels of data needed to describe and identify EFH: 1) distributional data; 2) density or relative abundance by habitat type 3); habitat-related growth, reproduction and survival; and, 4) productivity of different habitats (NMFS 2002). This call to attention of the importance of habitat in fishery management has since prompted many fisheries managers outside of federal fisheries to identify EFH within their waters.

Spotted seatrout, *Cynoscion nebulosus*, are one of the most highly sought recreational finfish species in Louisiana. An estimated 7.5 million spotted seatrout were harvested in Louisiana inland waters in 2004 (MRFSS 2005). Spotted seatrout, while considered a transient species, spends much of its life in the estuary (Arnold et al. 1976). Spotted seatrout are associated with oyster reefs, seagrass and marsh edge habitats (Lassuy 1983), although which habitats are essential to this species survival in this region is unknown. Despite this, a variety of artificial reef projects (i.e.; Coastal Conservation Association of Louisiana) have begun on the basis of anecdotal evidence that spotted seatrout prefer oyster shell habitat to other available habitats. While these projects are considered to be a natural solution to Louisiana’s marine habitat loss due to coastal erosion (CCA 2002), there is little evidence supporting the habitat preference of oyster shell to other available habitats by spotted seatrout in this region. Harding

and Mann (2001) found no difference in the habitat selection of spotted seatrout among sand bar, oyster shell bar and oyster reef habitats in the Piankatank River, Virginia. However, it was suggested that oyster reefs may be an important long-term habitat for juveniles of some transient species (Coen et al. 1999). Coen et al. (1999) concluded that the utilization of oyster reef habitats by commercially, recreationally and economically important species makes this habitat type essential, but the functional relationship remains to be evaluated.

Given the dramatic loss of marsh in the Barataria-Terrebonne Basin, and the ecological and economic importance of fisheries in this region, there is a need to address how fish use these declining habitats in this region. Therefore, data detailing the use and dependence of various habitat types is required to determine which habitats are supporting more spotted seatrout. The objective of this study was to examine the presence, relative abundance, biomass and length distribution of spotted seatrout among marsh edge, soft bottom and oyster shell habitats in Barataria Bay, LA, and to relate these measures to physical/chemical properties of the water, as a step towards identifying EFH for this species.

## **Methods and Materials**

### Study Area

All collections were made in Barataria Bay, part of the Barataria-Terrebonne Estuarine Basin (BTEB) in coastal Louisiana (Figure 1.1). The BTEB encompasses an area of approximately 16, 575 square kilometers within the Mississippi Deltaic Plain. The basin is bordered by the Mississippi River to the east, the East Atchafalaya Basin Levee and Atchafalaya River on the west and the Gulf of Mexico to the south. Three sites within Barataria Bay: Fisherman's Point (29°31'50"N 90°05'00"W), Manilla Village (29°25'74"N 89°59'20"W), and Grand Terre/Queen Bess (29°17'20"N 89°55'90"W/29°18'42"N 89°57'70"W respectively) were

sampled in order to characterize spotted seatrout in Barataria Bay. The salinity at these sites range from oligohaline to mesohaline to polyhaline among Fisherman's Point, Manilla Village, and Grand Terre/Queen Bess, respectively. These sites were chosen because they represented a range in salinity, and each contained the three habitat types of interest: marsh edge, soft bottom (mud/sand) and oyster shell. Since the Grand Terre site did not have oyster shell habitat, Queen Bess, a nearby location, was chosen to represent the oyster shell habitat for the polyhaline site. Although shell density differed at the three sites sampled, the within site variability was the comparison of interest. Klein digital side-scan sonar was used in an earlier study to differentiate oyster shell bottom from soft bottom (mud/sand). The swath format of the side-scan sonar provides a two dimensional acoustic image of bottom hardness (reflectance), surface texture (roughness) and topography. Habitat specific sampling locations were chosen from these side-scan surveys (Figures 1.2 to 1.5). In addition, SCUBA collections of bottom sediments were made to confirm the bottom type of habitats.

### Sampling Protocol

Monthly sampling began in May 2003 and was completed in May 2004, with the exception of December 2003, which was not sampled due to inclement weather. Physical/chemical properties of the water were collected at each site on each sampling trip. Data were collected about 30 cm below the water surface with a YSI model 85, and included water temperature (°C), dissolved oxygen (mg/L) and salinity (ppt). Physical/chemical data were collected only at the site level given the close proximity of habitat types within each site. Spotted seatrout were collected with a 46.5 m x 2.48 m gill net in the soft bottom and oyster shell habitat, and with a 46.5 m x 1.24 m gill net in the marsh edge habitat due to the shallower depth of the water at the marsh perimeter. All nets consisted of five 9.3 m panels, with the following

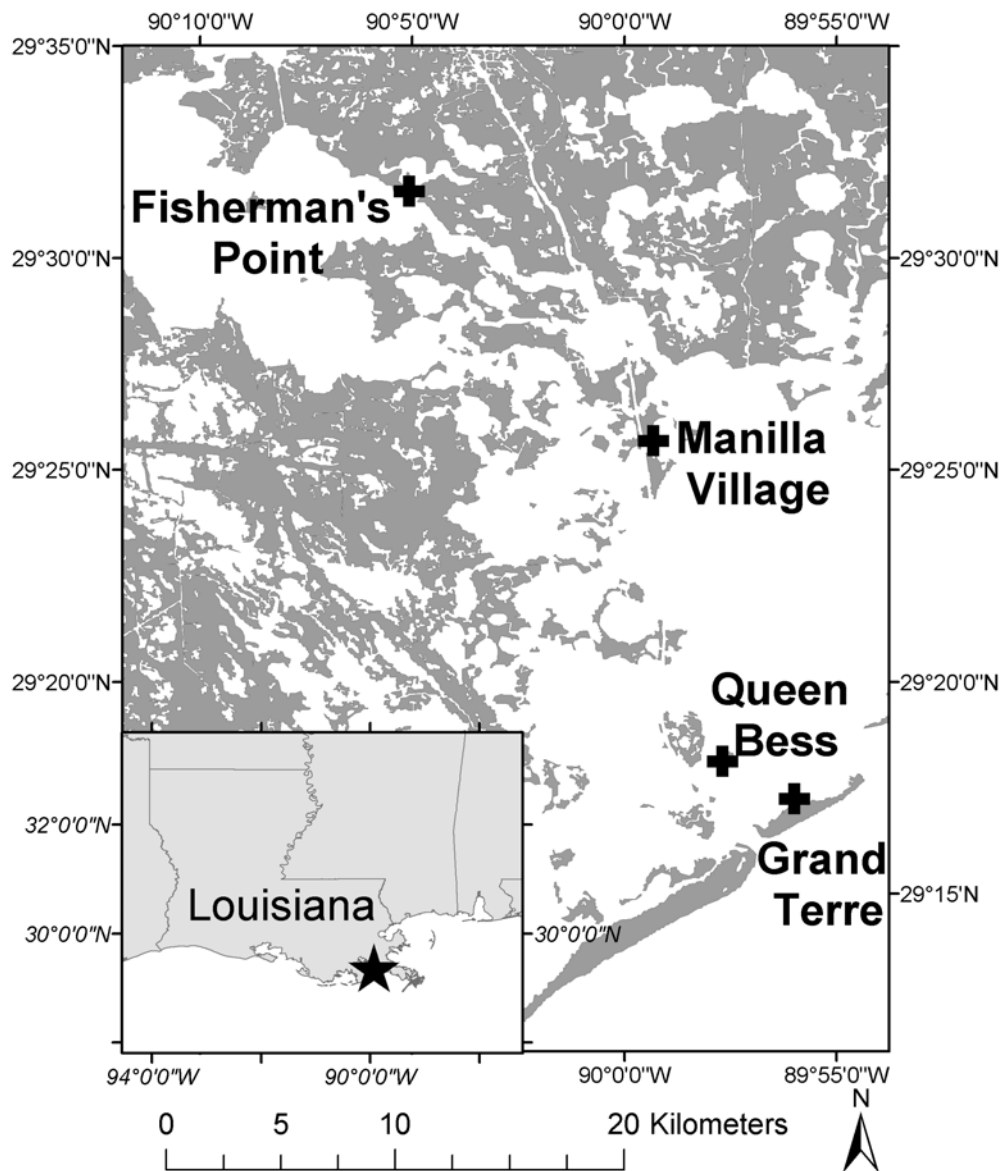


Figure 1.1. Map of Barataria Bay, Louisiana, and sampling sites: Grand Terre, Queen Bess, Manilla Village and Fisherman's Point.

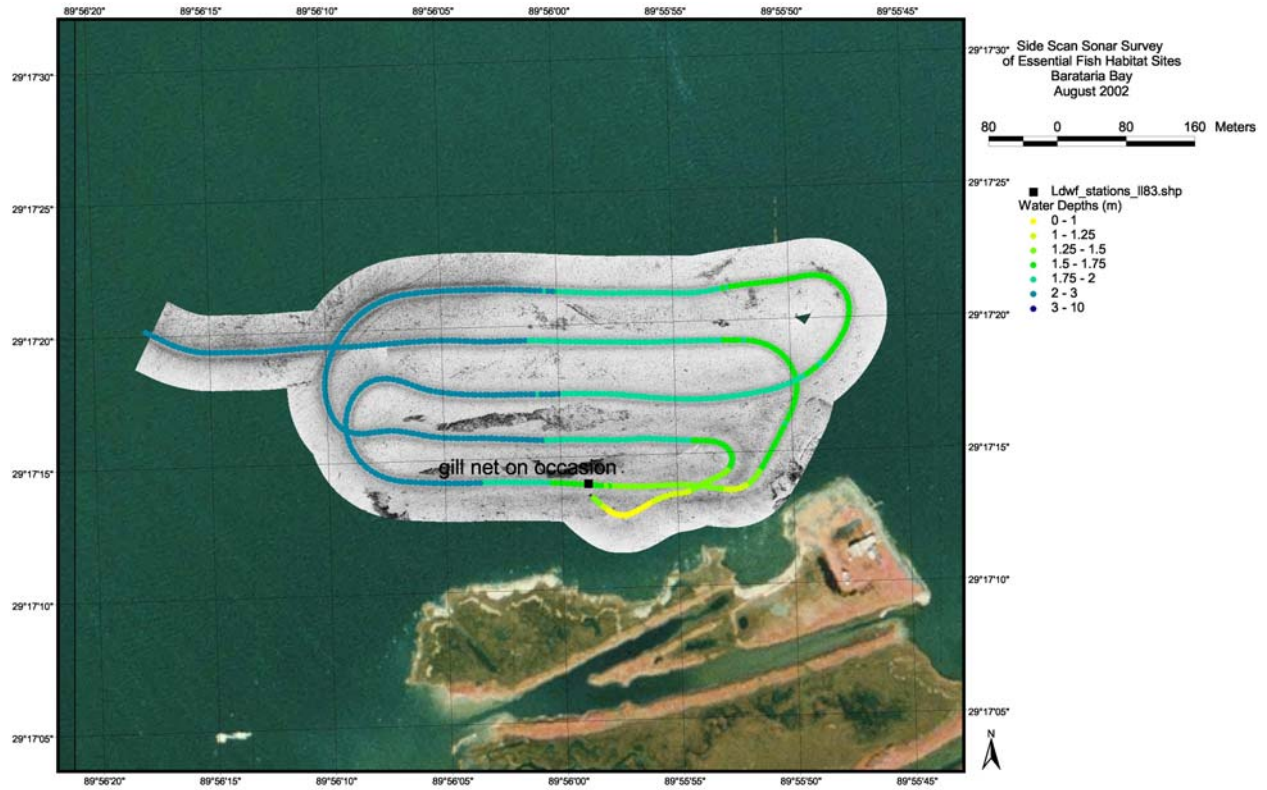


Figure 1.2. Side scan image of Grand Terre. Surface hardness is denoted by color (light areas indicate soft bottom and dark areas indicate hard bottom).

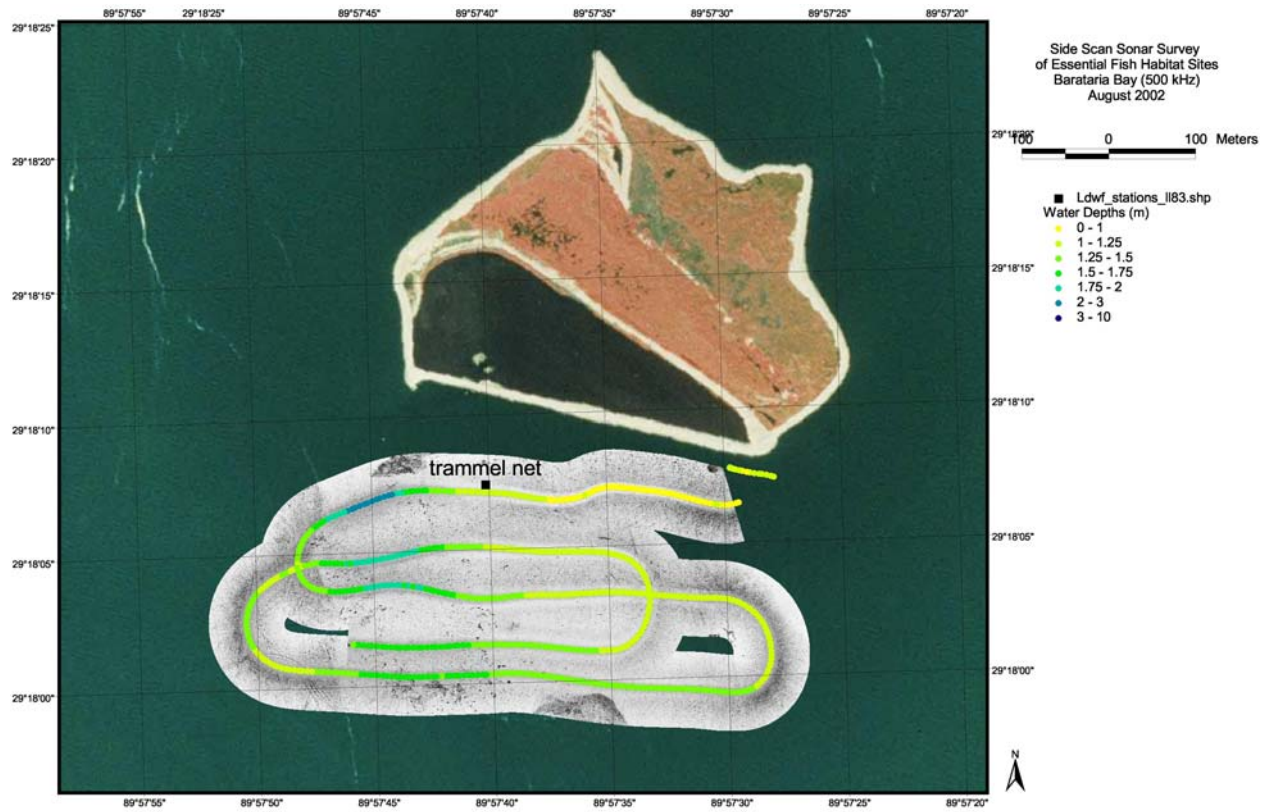


Figure 1.3. Side scan image of Queen Bess Island. Surface hardness is denoted by color (light areas indicate soft bottom and dark areas indicate hard bottom).

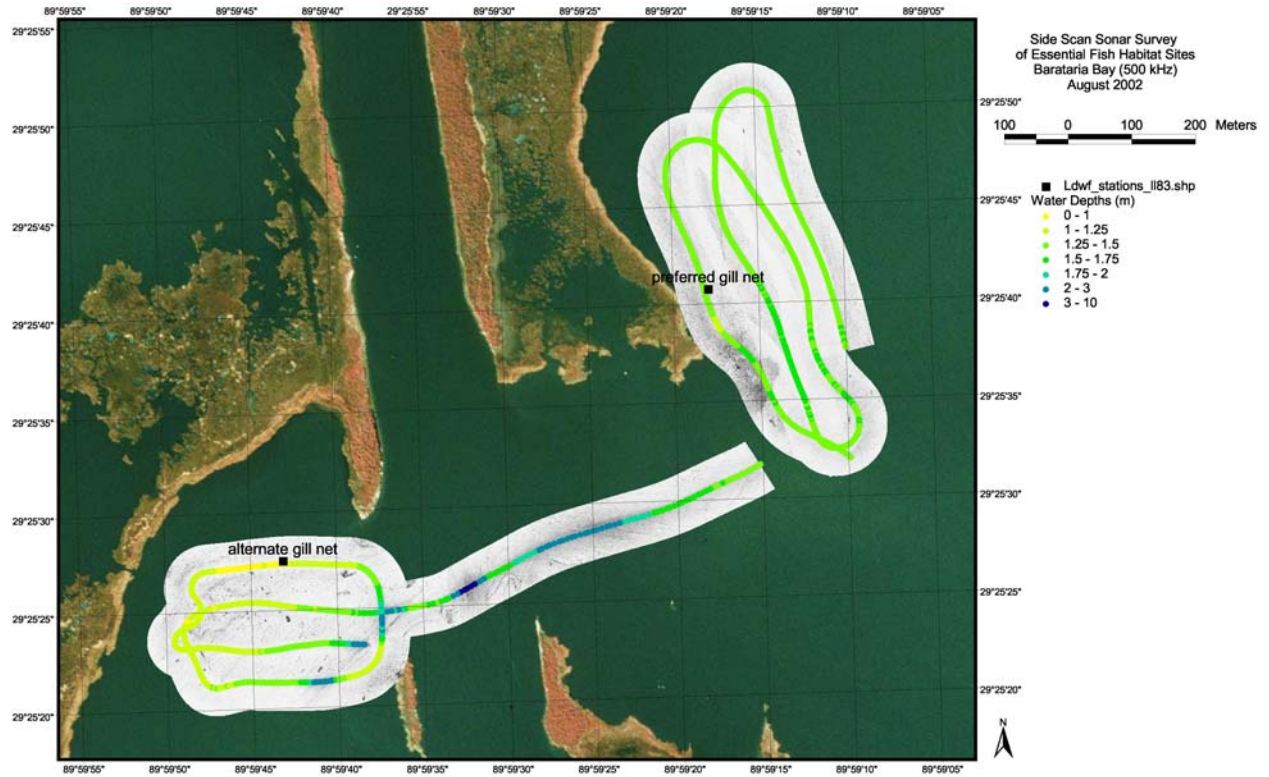


Figure 1.4. Side scan image of Manilla Village. Surface hardness is denoted by color (light areas indicate soft bottom and dark areas indicate hard bottom).

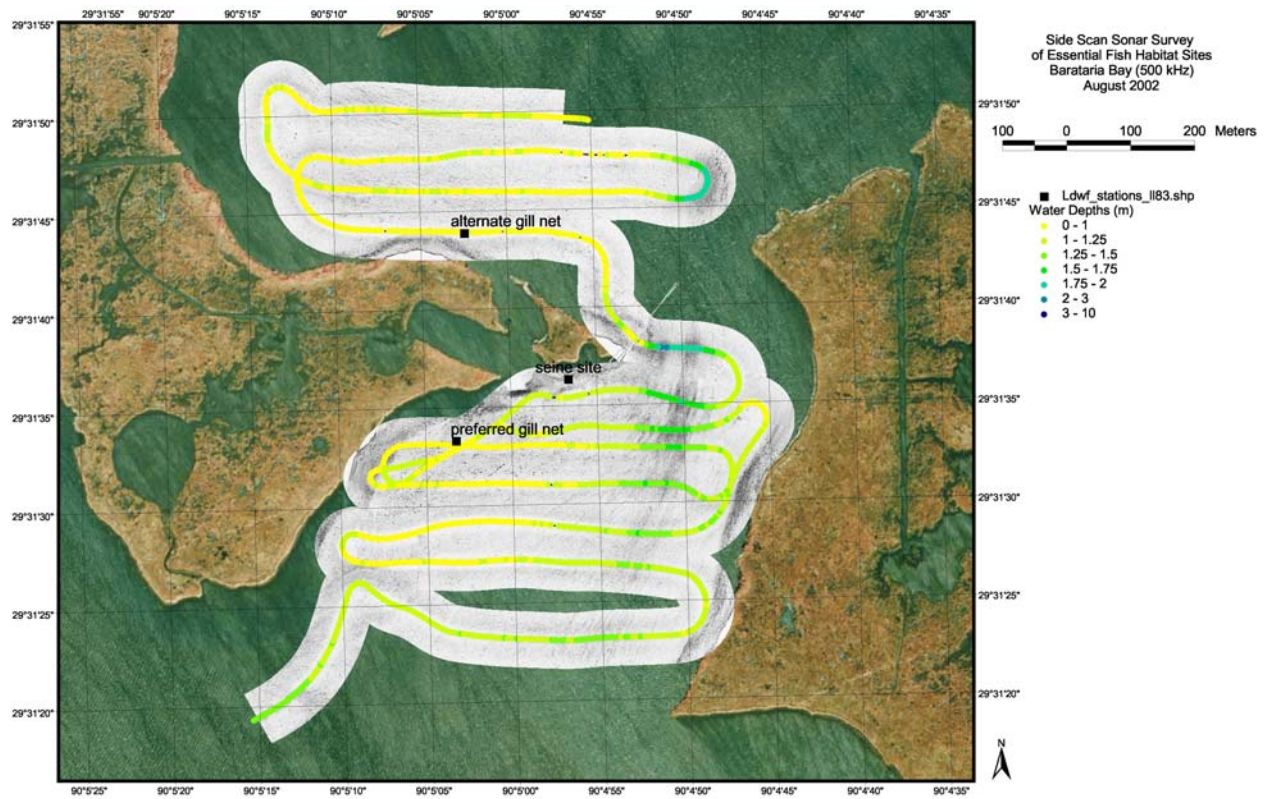


Figure 1.5. Side scan image of Fisherman's Point. Surface hardness is denoted by color (light areas indicate soft bottom and dark areas indicate hard bottom).

bar mesh sizes: 1.27, 1.91, 2.54, 3.18 and 3.81 cm. One gill net was set per habitat type per site for one hour. Fish were collected after one hour; then these nets were reset in the same place for another hour to replicate the sample in time. Fish collected were put in an ice slurry with MS 222, and then bagged and left on ice to be frozen later. In the laboratory spotted seatrout were weighed to the nearest tenth of a gram, measured for standard length (SL) to the nearest tenth of a centimeter and recorded by site and habitat.

### Statistical Analysis

Analysis of variance (ANOVA) (SAS Institute 2002) was used to test whether the physical/chemical properties of the water differed among sites and months. Variables that were significant at the level of  $\alpha=0.05$  were further tested with a Tukey HSD post-ANOVA test to determine which components of those variables accounted for differences detected in the ANOVA. Note that month was nested within year for this analysis because of the overlap between May 2003 and May 2004. ANOVA was also used to test whether the catch per unit effort (CPUE), biomass and standard length of spotted seatrout differed among habitats and sites, or in relation to the physical/chemical properties of the water, followed by Tukey HSD and least squared means post-ANOVA tests (SAS Institute 2002). In this analysis the variable month(year) was replaced by the covariables temperature, salinity and dissolved oxygen, since these factors differed significantly among months. A backward stepwise approach was used in this analysis, thus insignificant interactions were excluded from the model to maximize the power of the ANOVA. These interactions included temperature by site, salinity by site and dissolved oxygen by site. This simplified model (site, habitat, temperature, salinity, dissolved oxygen and site by habitat) was then used for all tests of significance. Normality of the CPUE and biomass data was tested with a Shapiro-wilks test, and by examining the residual and qq plot. CPUE and biomass

data were log (x+1) transformed because the raw data did not meet the normality assumption of an ANOVA. Finally, a logistic regression,  $\alpha=0.05$  (SAS Institute 2002), was used to predict the presence/absence of spotted seatrout based on habitat, site, and physical/chemical properties of the water. Due to time constraints and selection criteria of sampling sites, treatments were not replicated and therefore caution should be used when extrapolating results to areas other than those sampled during this project (Hurlbert 1984).

## **Results**

### Physical/Chemical Properties of the Water

Water temperature was highest between May and October, and ranged between 10.4°C and 32.1°C throughout the year (Figure 1.6). Temperature was inversely related to dissolved oxygen, which was highest between January and April, and ranged between 5.0 mg/L to 10.9 mg/L throughout the year (Figure 1.7). Temperature and dissolved oxygen did not differ significantly among sites ( $p = 0.06$ ,  $p = 0.68$ ; Table 1.1), but did differ among months sampled ( $p < 0.05$ ,  $p < 0.05$  respectively, Table 1.1). Salinity fluctuated throughout the year and ranged between 0.7 ppt to 29.6 ppt (Figure 1.8). Salinity differed significantly among sites ( $p < 0.05$ ; Table 1.1) and months sampled ( $p < 0.05$ ; Table 1.1). A Tukey HSD post-ANOVA test indicated that salinity at the Grand Terre and Queen Bess sites were not significantly different from one another, which validated the inclusion of Queen Bess as a substitute shell habitat for the Grand Terre site (Table 1.2). In addition, the Tukey HSD post-ANOVA test significantly separated the polyhaline sites Grand Terre and Queen Bess from the mesohaline site Manilla Village and the oligohaline site Fisherman's Point (Table 1.2).

## Catch Data

I collected 176 spotted seatrout between May 2003 and May 2004. Of these, 90 were collected from the Grand Terre/Queen Bess site (30 at marsh edge, 38 at soft bottom and 22 at oyster shell), 71 were collected from Manilla Village (6 at marsh edge, 24 at soft bottom and 41 at oyster shell) and 15 were collected from Fisherman's Point (5 at marsh edge, 3 at soft bottom and 7 at oyster shell) (Table 1.4, Figures 1.9 to 1.11). There was no overall significant difference in CPUE between habitat types ( $p = 0.21$ , Table 1.1). In general, more spotted seatrout were collected at the oyster shell habitat followed by soft bottom and then marsh edge. Catch significantly differed among sites ( $p < 0.01$ , Table 1.1). A Tukey HSD post-ANOVA test detected that CPUE was significantly higher at Grand Terre/Queen Bess and Manilla Village than at Fisherman's Point (Table 1.2). CPUE was also significantly related to temperature ( $p = 0.01$ , Table 1.1) and salinity ( $p = 0.04$ , Table 1.1), and increased as both temperature and salinity increased (Figure 1.12). There was no significant relationship between CPUE and dissolved oxygen ( $p = 0.86$ ; Table 1.1).

The biomass and standard length of spotted seatrout were significantly different between habitat types ( $p < 0.05$  and  $p < 0.05$  respectively, Table 1.1), with larger spotted seatrout at the oyster shell habitat compared to marsh edge and soft bottom (Table 1.4). However, this was not supported by a Tukey HSD post-ANOVA test (Table 1.2), which is likely due to the significant interaction between site and habitat ( $p < 0.05$ , Tables 1.1 and 1.3). The exclusion of the Grand Terre/Queen Bess from this comparison resulted in smaller spotted seatrout collected along the marsh edge as compared to the soft bottom and oyster shell habitat (Table 1.4). Moreover, the biomass and standard length of spotted seatrout differed significantly among sites ( $p < 0.05$  and  $p < 0.05$  respectively, Table 1.1). A Tukey HSD post-ANOVA test indicated that spotted seatrout

Table 1.1. Results from analysis of variance comparing water temperature, dissolved oxygen and salinity by site and months, and CPUE, biomass and standard length of spotted seatrout by habitat, site, water temperature, dissolved oxygen and salinity.

	d.f.	F	MS	p-value
<b>Temperature</b>				
Site	3	2.69	2.26	0.06
Month(year)	11	177.48	149.17	<0.05
<b>Salinity</b>				
Site	3	111.68	518.92	<0.05
Month(year)	11	16.38	76.09	<0.05
<b>Dissolved oxygen</b>				
Site	3	0.50	0.36	0.68
Month(year)	11	11.95	8.52	<0.05
<b>Catch per unit effort</b>				
Habitat	2	1.58	0.50	0.21
Site	2	7.58	2.38	<0.05
Temperature	1	5.65	1.79	0.02
Dissolved oxygen	1	0.03	0.01	0.86
Salinity	1	4.43	1.39	0.04
Site x habitat	4	1.96	0.62	0.10

Table 1.1 Cont'd.

Biomass	d.f.	F	MS	p-value
Habitat	2	19.96	6.26	<0.05
Site	2	5.24	1.83	<0.05
Temperature	1	14.78	5.15	<0.05
Dissolved oxygen	1	3.14	1.09	0.08
Salinity	1	1.76	0.61	0.19
Site x habitat	4	14.76	5.14	<0.05

Length	d.f.	F	MS	p-value
Habitat	2	13.71	262.88	<0.05
Site	2	5.02	96.32	<0.05
Temperature	1	6.92	132.61	0.01
Dissolved oxygen	1	3.14	60.11	0.08
Salinity	1	3.26	62.57	0.07
Site x habitat	4	12.43	238.28	<0.05

Table 1.2. Results from Tukey HSD post-ANOVA test comparing water temperature, dissolved oxygen and salinity by site and months, and comparing CPUE, biomass and standard length of spotted seatrout by habitat and site.

Temperature	Tukey HSD	Mean	N	Site/habitat
	A	24.8	12	Grand Terre
	A	24.7	12	Queen Bess
	A	24.1	12	Manilla Village
	A	23.9	11	Fisherman's Point

Table 1.2 Cont'd.

Dissolved Oxygen	Tukey HSD	Mean	N	Site/habitat
	A	7.6	12	Grand Terre
	A	7.4	12	Queen Bess
	A	7.2	12	Manilla Village
	A	7.2	11	Fisherman's Point
Salinity				
	A	19.6	12	Grand Terre
	A	19.3	12	Queen Bess
	B	11.3	12	Manilla Village
	C	4.8	11	Fisherman's Point
Log (CPUE + 1)				
	A	0.46	70	Grand Terre/Queen Bess
	A	0.44	71	Manilla Village
	B	0.14	66	Fisherman's Point
Log (CPUE + 1)				
	A	0.27	68	Marsh edge
	A	0.35	69	Soft bottom
	A	0.44	70	Oyster shell
Log (Biomass + 1)				
	A	5.4	90	Grand Terre/Queen Bess
	AB	5.1	72	Manilla Village
	B	4.8	14	Fisherman's Point

Table 1.2 Cont'd.

Log (Biomass + 1)	Tukey HSD	Mean	N	Site/habitat
	A	5.1	42	Marsh edge
	A	5.2	65	Soft bottom
	A	5.3	68	Oyster shell
SL				
	A	25.4	90	Grand Terre/Queen Bess
	AB	23.3	72	Manilla Village
	B	22.0	14	Fisherman's Point
	A	23.8	42	Marsh edge
	A	23.4	65	Soft bottom
	A	25.3	69	Oyster shell

Table 1.3. Results from Tukey HSD post-2 way ANOVA test of effects comparing SL and biomass by site and habitat. Different letters indicate a significant difference.

SL	Marsh edge	Soft bottom	Oyster shell
Grand Terre/Queen Bess	25.88±0.83 AC	21.33±0.83 BDE	27.57±1.07 A
Manilla Village	16.43±1.68 D	24.98±0.98 ABC	24.95±0.77 ABC
Fisherman's Point	17.75±2.07 CDE	30.57±2.89 AB	25.72±2.19 ABCD
Biomass	Marsh edge	Soft bottom	Oyster shell
Grand Terre/Queen Bess	5.44±0.11 A	4.89±0.11 BC	5.63±0.14 A
Manilla Village	3.94±0.23 D	5.39±0.13 AB	5.37±0.10 AB
Fisherman's Point	4.10±0.28 CD	6.08±0.39 AB	5.14±0.29 ABCD

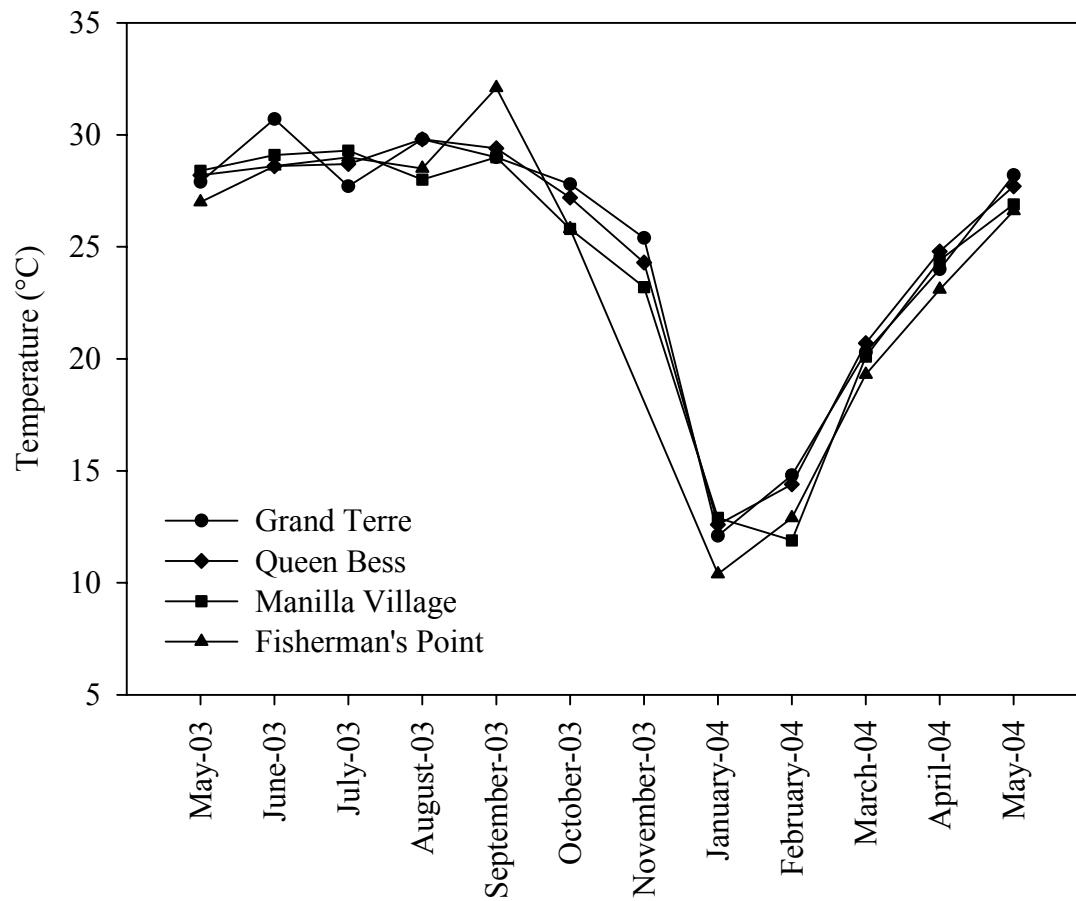


Figure 1.6. Water temperature (°C) by site and month from May 2003 to May 2004.

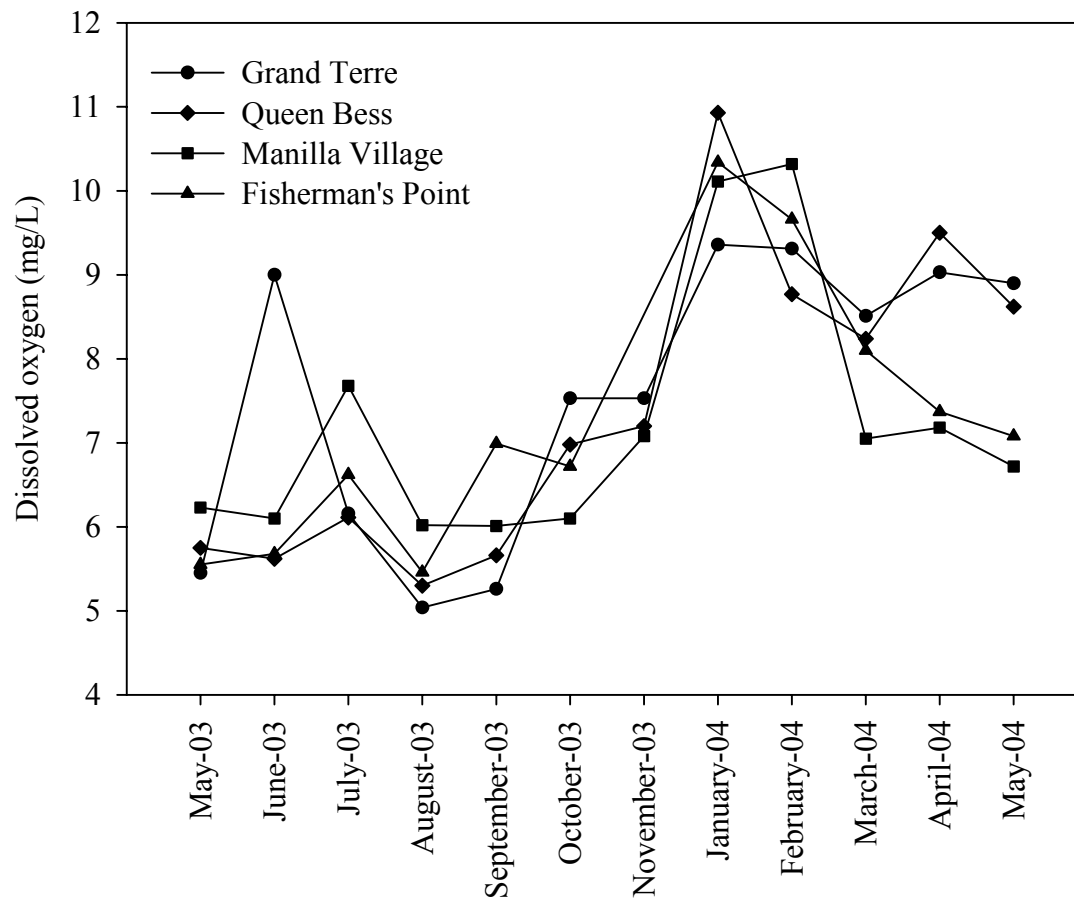


Figure 1.7. Dissolved oxygen (mg/L) by site and month from May 2003 to May 2004.

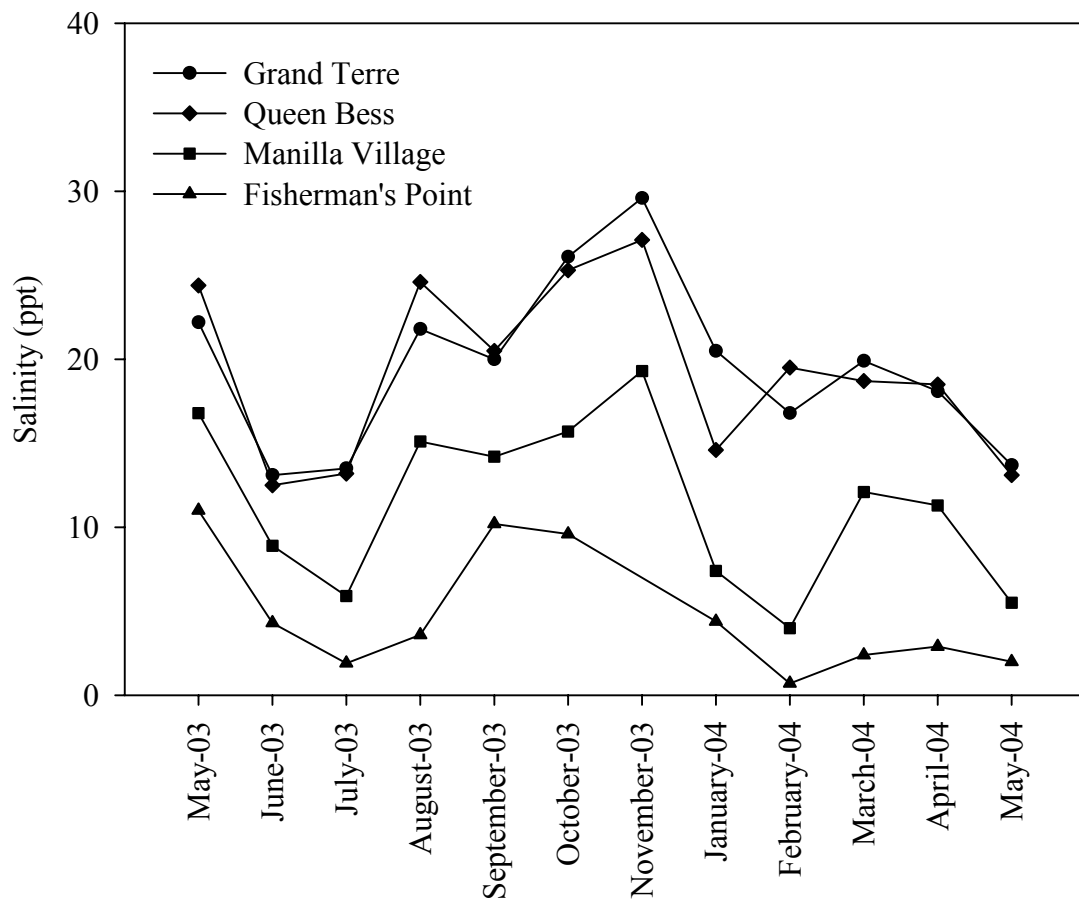


Figure 1.8. Salinity (ppt) by site and month from May 2003 to May 2004.

Table 1.4. Summary of total catch, mean biomass and mean standard length of spotted seatrout by site and habitat, as well as an overall mean of biomass and standard length for each site and habitat.

	Grand Terre/ Queen Bess	Manilla Village	Fisherman's Point	Overall Mean by Habitat
<b>Total Catch</b>				
Marsh	30	6	5	
Soft Bottom	38	24	3	
Oyster shell	22	41	7	
<b>Mean Biomass</b>				
Marsh edge	286.2	81.7	92.0	229.0
Soft bottom	170.5	211.8	366.7	198.1
Oyster shell	373.5	221.2	152.4	263.8
Overall Mean	258.7	207.5	176.8	
<b>by Site</b>				
<b>Mean Length</b>				
Marsh edge	26.6	16.4	17.7	23.8
Soft bottom	22.5	24.2	28.1	23.4
Oyster shell	28.7	23.9	22.6	25.3
Overall Mean	25.4	23.3	22.0	
<b>by Site</b>				

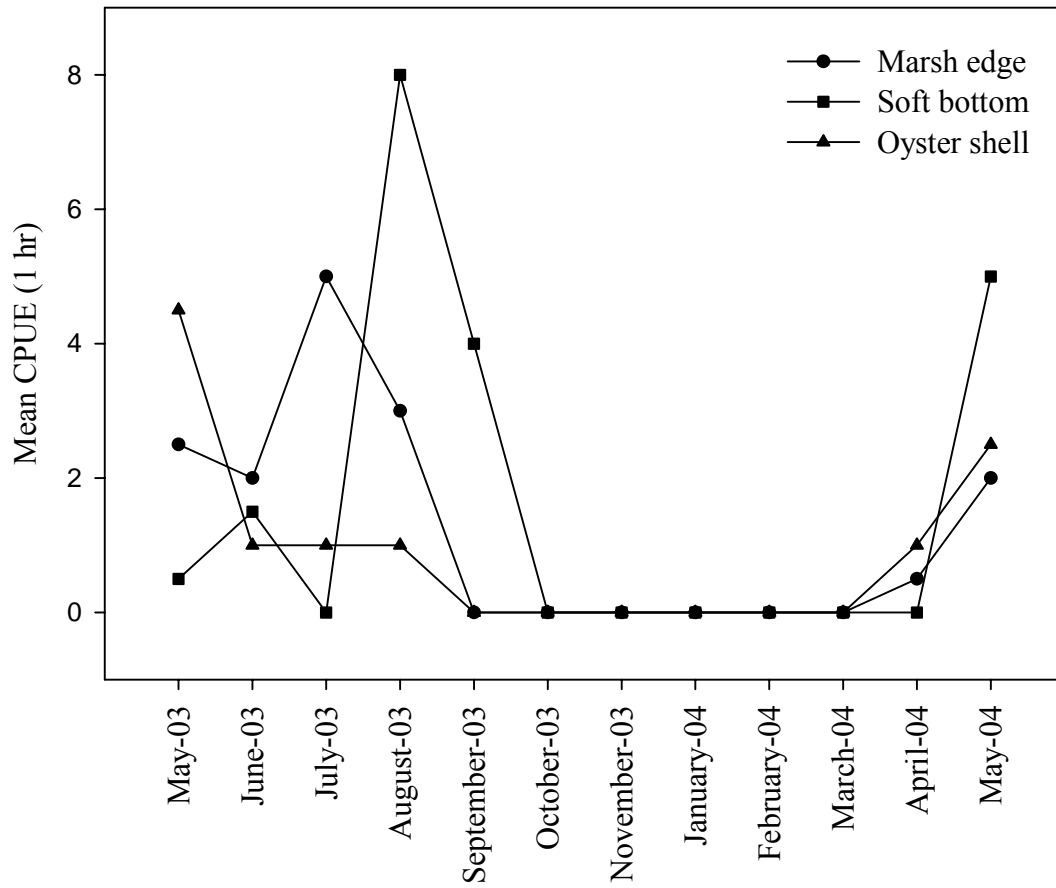


Figure 1.9. Catch per unit effort of spotted seatrout at Grand Terre/Queen Bess by habitat type from May 2003 to May 2004.

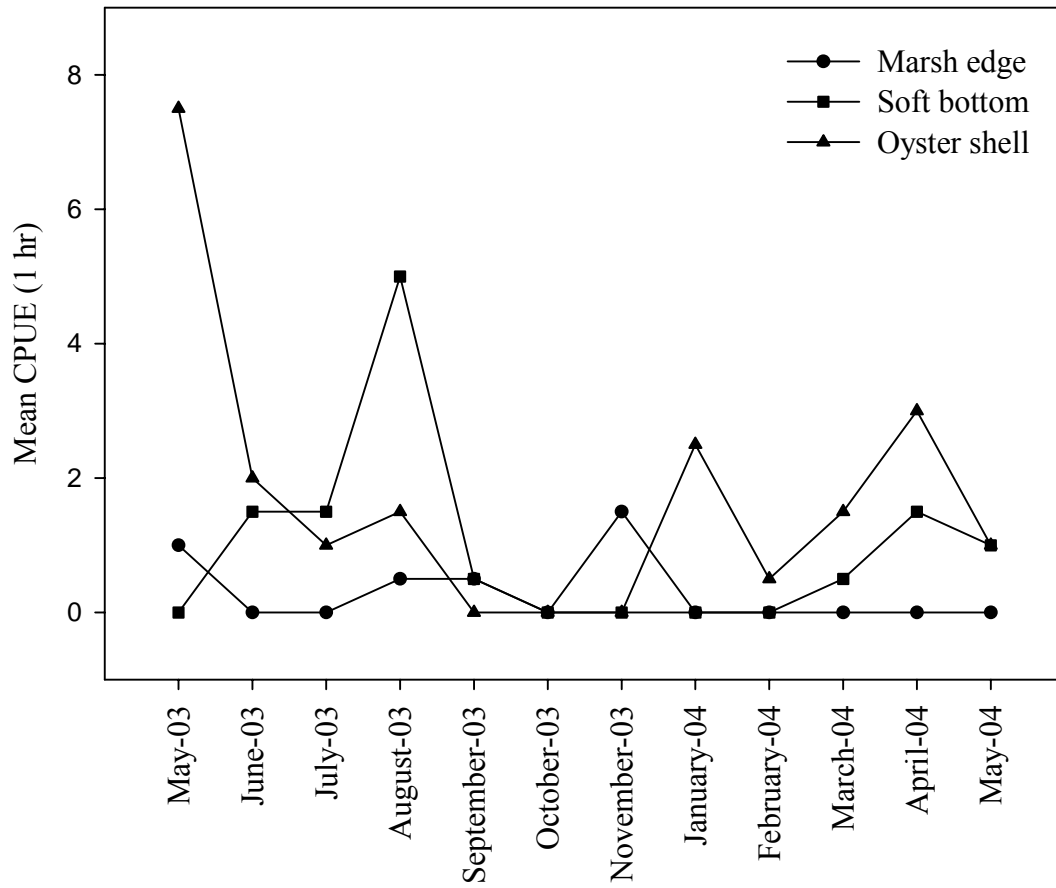


Figure 1.10. Catch per unit effort of spotted seatrout at Manilla Village by habitat type from May 2003 to May 2004.

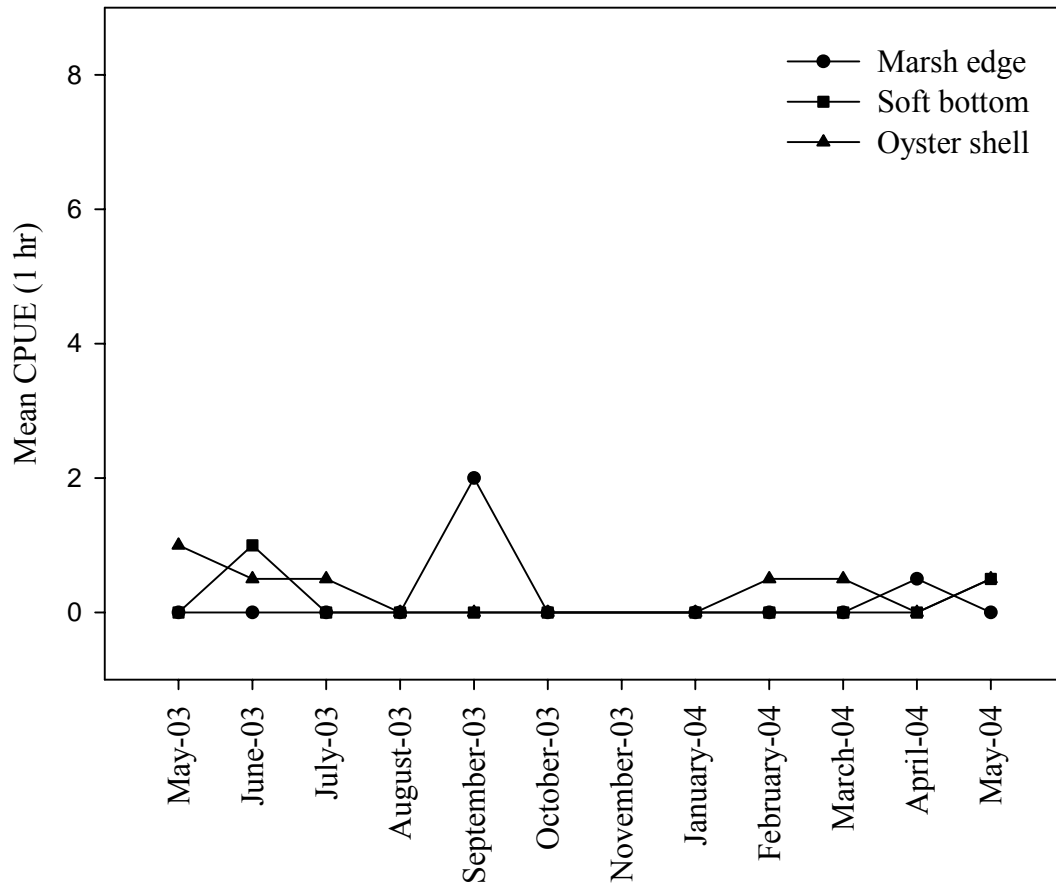


Figure 1.11. Catch per unit effort of spotted seatrout at Fisherman's Point by habitat type from May 2003 to May 2004.

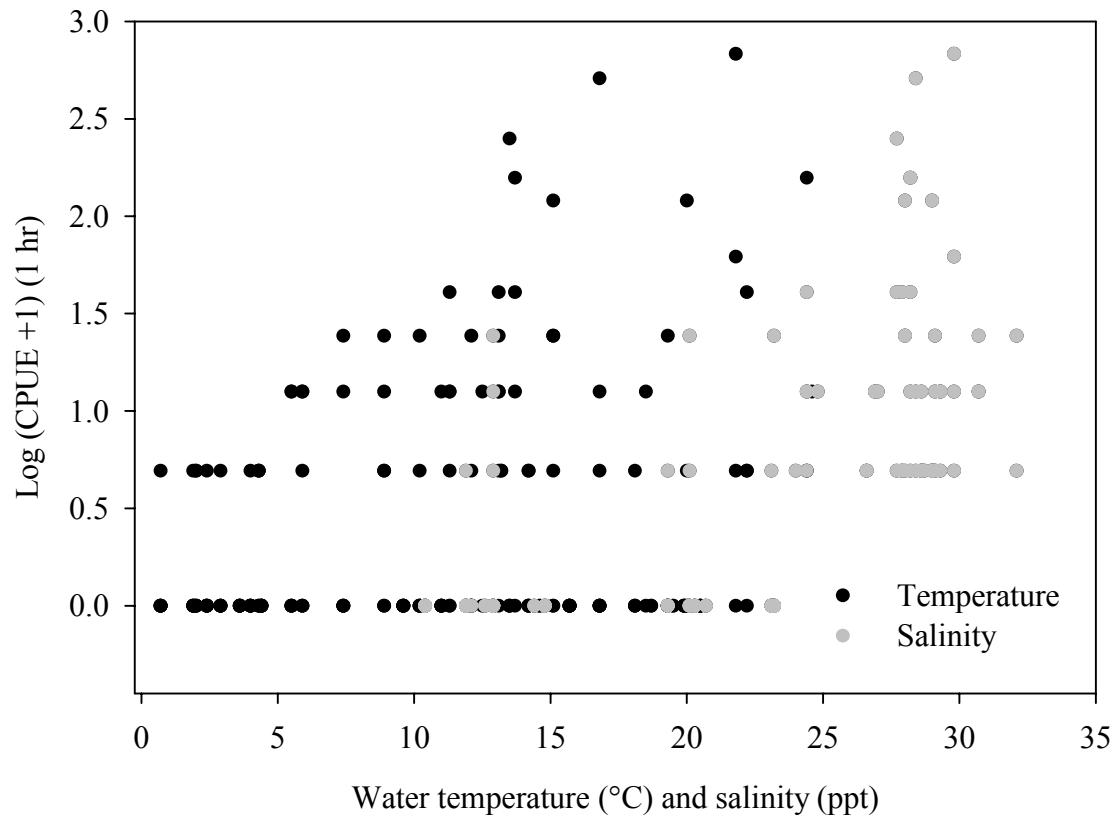


Figure 1.12. Relationship between log (CPUE +1) of spotted seatrout and water temperature (°C) and salinity (ppt) for all sites combined from May 2003 to May 2004.

were significantly larger at Grand Terre/Queen Bess compared to Fisherman's Point, but that spotted seatrout from Manilla Village were not significantly different from either site (Table 1.2), however there was a significant interaction between site and habitat indicating that the main effects were not consistent (Table 1.2). Thus spotted seatrout were generally larger when the salinity was relatively high. There also was a significant relationship between biomass and standard length of spotted seatrout and water temperature ( $p < 0.05$  and  $p = 0.01$  respectively, Table 1.1), with biomass and standard length increasing as water temperature increased (Figures 1.13 and 1.14 respectively).

Logistic regression was used to predict the probability of detecting the presence of spotted seatrout by site, habitat, temperature, dissolved oxygen and salinity and all interactions. The model was significant at  $\alpha=0.05$ , and included habitat, temperature and the habitat x temperature interaction, with an odds ratio of 1.55 to 1.14 (Table 1.5). The predicted probabilities of presence based on habitat and temperature are presented in Figures 1.15 and 1.16 respectively. The probability of detection increased from 86.0% to 99.8% to 99.9% as you moved from the marsh edge to soft bottom to oyster shell habitat. Thus the probability of detecting a spotted seatrout was almost 14% more likely over oyster shell and soft bottom than at the marsh edge. The probability of detection for spotted seatrout also increased as water temperature increased. As water temperature increased from 10.4°C to 14.8°C, the probability of detection increased from 32.6% to 82.6%. The probability of detecting a spotted seatrout reached 98% at 19.3°C and 99.0% as the water temperature reached 24°C and greater. Therefore, one is more likely to find a spotted seatrout in the warmest months of the year, May through October, although it is possible to encounter a spotted seatrout between November and April. The significant interaction between habitat and temperature suggests that one is most likely to find a

spotted seatrout in open water, either over oyster shell or soft bottom, compared to the marsh edge, particularly when the water temperatures are 24.0°C and greater.

Table 1.5. Results from the logistic regression of spotted seatrout, including only those variables significant at the alpha=0.05 level (habitat and temperature).

	Chi-square	d.f.	p-value	Odds ratio estimate
Model	11.30	4	<0.05	
Habitat	7.87	1	<0.05	1.55
Temperature	9.80	1	<0.05	1.14
Habitat x temperature	6.82	1	0.01	

## Discussion

Numerous studies have shown that the density of fish differs between habitat types, many of which have focused on vegetated versus non-vegetated habitats (Crowder and Cooper 1982; Orth et al. 1984; Pollard 1984; Zimmerman et al. 1984; Baltz et al. 1993; Rozas and Zimmerman 2000). Although, a few studies have focused on the importance of oyster shell habitat and how it compares to adjacent soft bottom habitats (Coen et al. 1999; Harding and Mann 2001; Lehnert and Allen 2002) and even fewer have compared oyster shell to both soft bottom and vegetated habitats (Stunz and Minello 2001; Stunz et al. 2002). Despite this, there are a number of restoration projects underway in Louisiana building artificial reefs based on anecdotal evidence that recreationally important species such as the spotted seatrout prefer oyster shell habitat to other available habitats. The literature does suggest that subtidal oyster shell bottoms are critical habitat for some fish (Lehnert and Allen 2002). Lehnert and Allen (2002) found that subtidal oyster shell habitats supported a more diverse and abundant demersal fish population than nearby

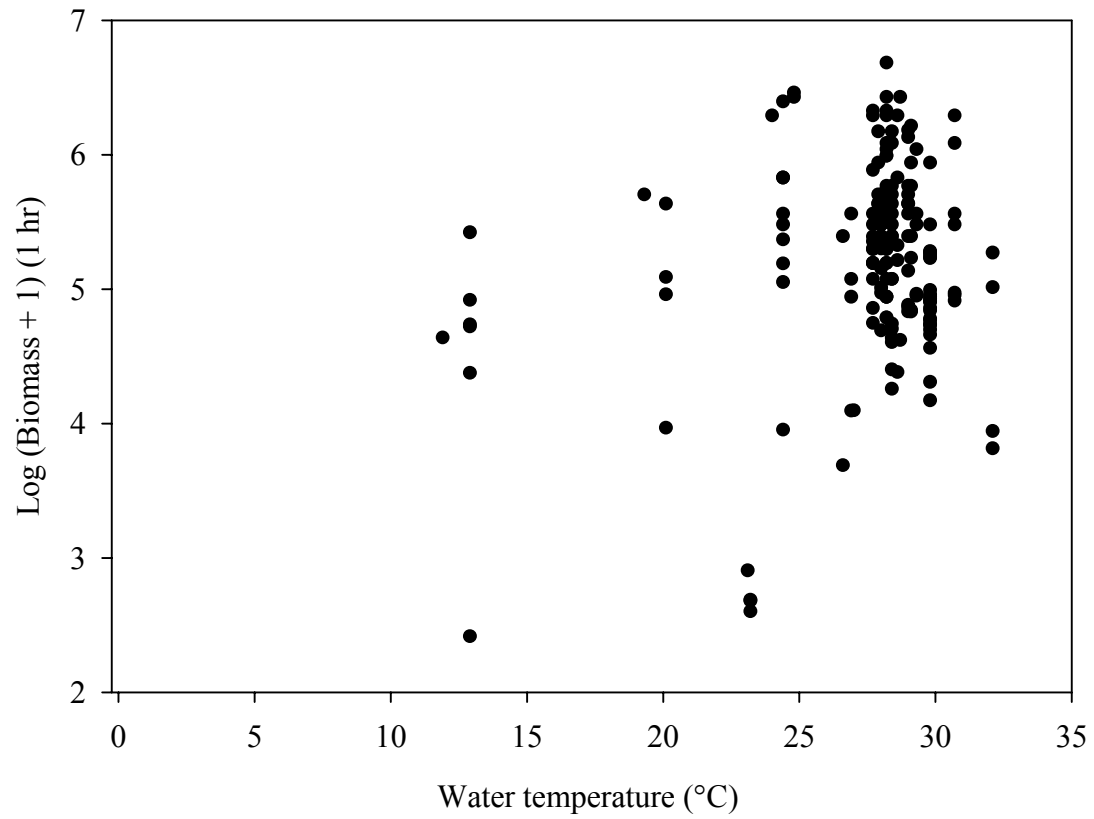


Figure 1.13. Relationship between log (biomass +1) of spotted seatrout and water temperature (°C) for all sites combined from May 2003 to May 2004.

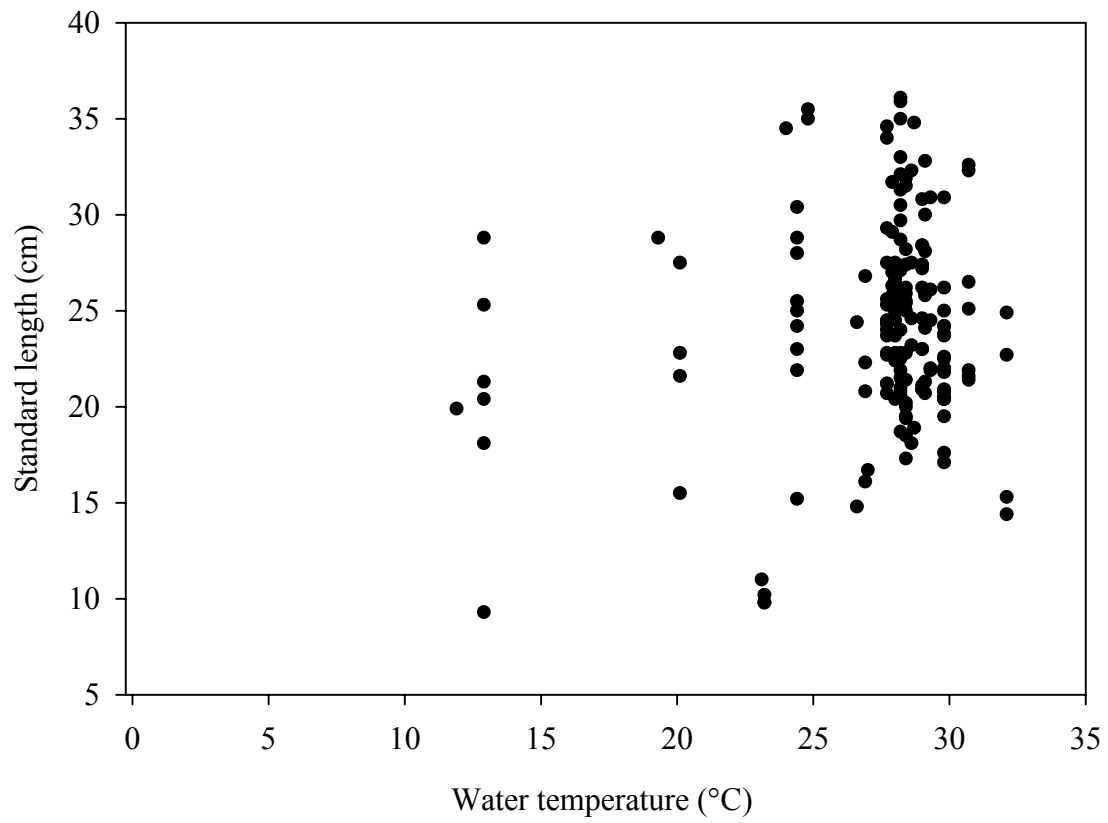


Figure 1.14. Relationship between standard length of spotted seatrout water temperature (°C) for all sites combined from May 2003 to May 2004.

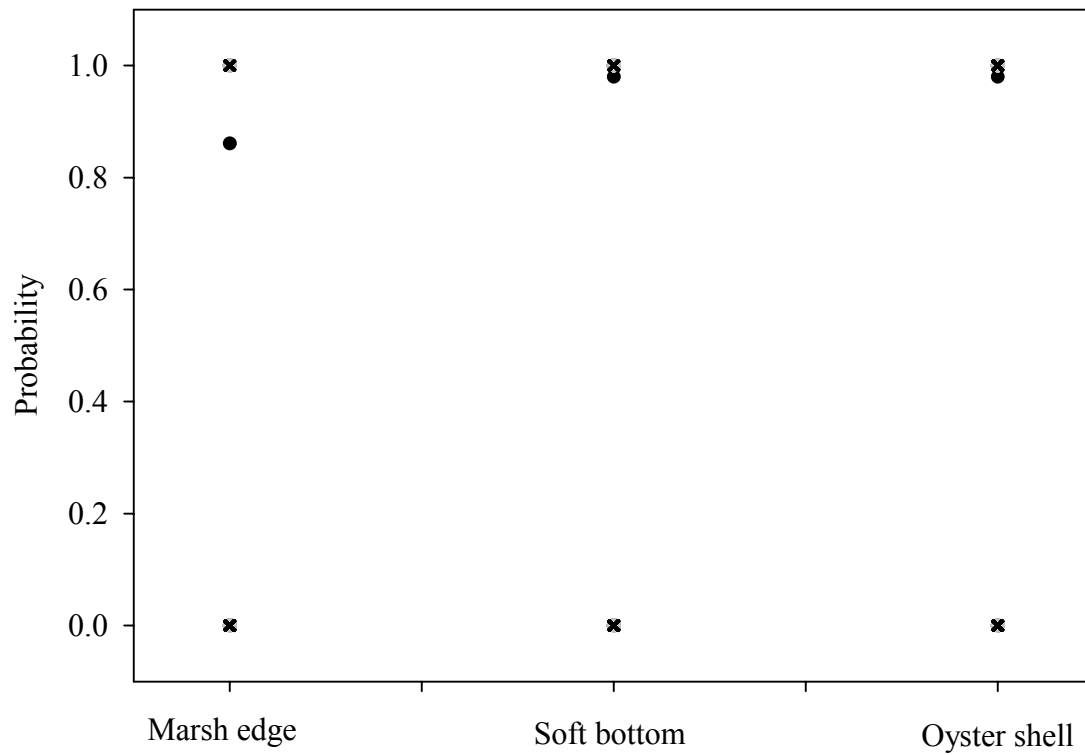


Figure 1.15. Logistic regression of spotted seatrout presence/absence by habitat. Closed circles represent predicted probabilities and asterisks represent presence.

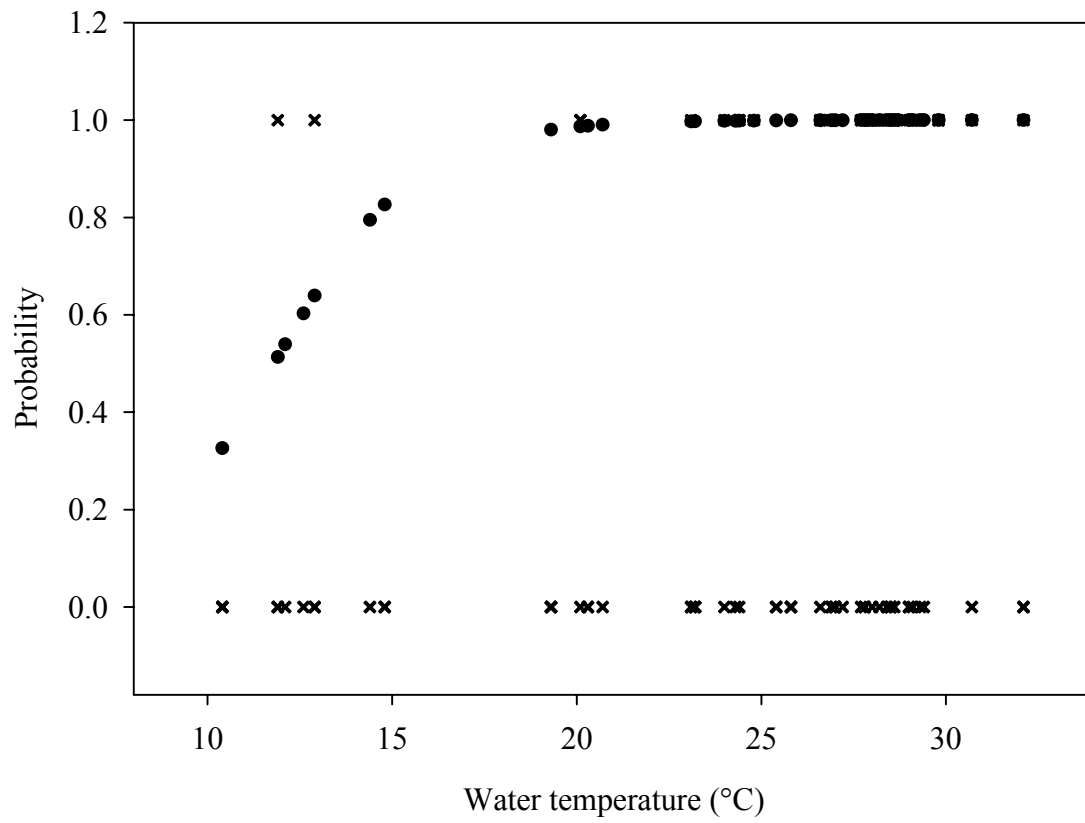


Figure 1.16. Logistic regression of spotted seatrout presence/absence by water temperature. Closed circles represent predicted probabilities and asterisks represent presence.

soft bottom habitats. This may be because oyster shell habitats provide greater structural complexity than adjacent soft bottom habitats, and because more complex habitats offer a greater amount of refuge and are often selected over less complex habitats, especially in the presence of predators (Jordan et al 1996).

In this study, spotted seatrout showed no consistent pattern of habitat selection among marsh edge, soft bottom and oyster shell. While more spotted seatrout were collected at the oyster shell habitat, followed by soft bottom and marsh edge respectively, this pattern was not true for all sites sampled. These results are similar to Harding and Mann (2001) who found that catches of spotted seatrout were similar across habitats sampled, which included oyster shell reef, oyster shell bar and sand bar. However, Perret et al. (1980) tied the distribution of spotted seatrout to food availability and stated that spotted seatrout are likely found in any area offering suitable salinity and temperature regimes with sufficient prey availability. A review of factors influencing habitat selection of fishes in marsh ecosystems by Craig and Crowder (2000) suggests that habitat selections of organisms over their ontogeny are an integrated response to their biotic and abiotic environment, presumably resulting in the selection of habitats that enhance fitness.

Differences in CPUE of spotted seatrout in this study were partially defined by physical/chemical properties of the water. The relative abundance of spotted seatrout increased as temperature and salinity increased, and was greatest at the mesohaline and polyhaline sites. These results support Kostecki and Fore (1984) who found that spotted seatrout prefer mesohaline and polyhaline portions of estuaries to oligohaline portions, and water temperatures between 20°C and 32°C. The relative abundance of spotted seatrout did not depend on dissolved oxygen concentrations in the water, and this was likely due to the fact that dissolved oxygen

never reached threshold levels and therefore was never at levels that would restrict habitat use by spotted seatrout (Clark et al. 2003). Craig and Crowder (2000) stated that abiotic factors such as temperature, salinity and dissolved oxygen can have direct physiological effects on metabolism. However, they point out that most fish are tolerant of a wide range in abiotic conditions and that this should be particularly true for species that have evolved in a fluctuating environment (marsh residents) or migrate between estuarine and coastal environments (marsh transients). Although, it is possible that the catchability of spotted seatrout in the gill nets was influenced by spatial and temporal differences in the physical/chemical properties of the water. Gill nets are known to be influenced by numerous variables including water temperature, time of day, water level fluctuations, turbidity and currents (Hubert 1996). Moreover, gill nets are influenced by seasonal patterns in the movement and distribution of fish that occur as a result of spawning activity, habitat requirements and food availability (Hubert and O'Shea 1992).

The biomass and standard length distribution of spotted seatrout in this study indicate that spotted seatrout were generally larger over the soft bottom and oyster shell habitats as compared to the marsh edge habitat. Body size of fish can play a large role in determining fish-habitat interactions (Persson and Crowder 1998) and fish often exhibit ontogenetic habitat shifts (Werner and Gilliam 1984). Studies have shown that spotted seatrout prefer marsh edge habitat as juveniles (Minello 1999). The smallest mesh size of the gill nets was 1.27 cm stretched mesh, therefore the gill net was not selecting for fish as small as newly settled spotted seatrout. Nonetheless, young-of-the-year spotted seatrout were caught in this study. Therefore while I cannot discuss the importance of marsh edge habitat to newly settled spotted seatrout, results indicate that there was a trend to catch smaller spotted seatrout at the marsh edge compared to soft bottom and oyster shell habitats. The exception to this trend was at Grand Terre/Queen Bess, the

site closest to the mouth of the estuary, which was likely due to the fact that a large number of large gravid females were collected near the marsh edge at this site. Spotted seatrout are known to spawn near the mouth of the estuary in close proximity to barrier islands and the passes between them connecting the estuary to the Gulf of Mexico (Ditty 1984).

The biomass and standard length of spotted seatrout were generally greater when the water temperature was warmer and the salinity was higher. Spotted seatrout are known to spend their entire life cycle near or in estuaries, which provide habitat for all early life stages, juveniles and adults (Tab 1966). It is unclear why the spotted seatrout were larger near the mouth of the estuary, but it may be that the older spotted seatrout are closer to the mouth of the estuary while the younger spotted seatrout are further up in the estuary. Hestler et al. (1993) found that the size of spotted seatrout was not uniform across all estuarine zones at some times in the year. They found that the abundance of recruit and spawner spotted seatrout were greatest in the lower estuarine zone (15-30 ppt) during the spawning season (May-August). When spawning was complete (September-December), spawners were uniformly distributed across the estuary while the new recruits were more abundant in the upper estuary (0-9 ppt).

There was little difference in the ability to predict the presence of spotted seatrout among the different habitat types, although they were predicted to be about 14% more likely to be found over oyster shell and soft bottom than near the marsh edge. Spotted seatrout are highly mobile and these results likely reflect that these seatrout are moving among habitat types while foraging. The ability to predict the presence of spotted seatrout was greatest based on water temperature, increasing from 32.6 % to 82.6% when the water temperature increased from 10.4°C to 14.3°C, and reaching 99.9% at 24.0°C and greater. Moreover, there was a significant interaction between habitat and temperature. Therefore in the most general sense, spotted seatrout are more likely to

be found in the open water, regardless of oyster shell or soft bottom, when the water temperature is 24.0°C and greater. Moreover, because larger spotted seatrout were collected when the water temperatures were 24.0°C and greater, the best place and time to catch a large spotted seatrout in Barataria Bay is in the open water when the water temperature is at or above 24°C.

While I applaud the NMFS for highlighting the importance of habitat use in fishery management as part of the Sustainable Fisheries Act, this study has demonstrated that identifying which habitats are essential for a given species may not be possible based on the first few guidelines provided by NMFS. This study illustrates that the habitat preference of spotted seatrout is not easily defined by habitat type alone, but rather that their distribution, relative abundance, biomass and length distribution are more likely determined by a combination of habitat and physical/chemical properties of the water. The CPUE increased as water temperature and salinity increased, although there appears to be little preference of oyster shell over soft bottom or marsh edge habitats by adult spotted seatrout. Although, the smaller spotted seatrout were generally more abundant near the marsh edge habitat. Therefore, it is difficult to define any of these habitats individually as essential for spotted seatrout. It is more likely that together these habitats make up an ecosystem that is important for spotted seatrout, although it appears that the marsh edge habitat is particularly important to juvenile spotted seatrout. Thus restoration efforts to restore the wetlands in coastal Louisiana will only help this species by maintaining the integrity of this important ecosystem, while efforts to build artificial reefs may not have all of the anticipated benefits for spotted seatrout.

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## CHAPTER 2: EXAMINING THE FOOD WEB DYNAMICS OF SPOTTED SEATROUT, *CYNOSCION NEBULOSUS*, AMONG MARSH EDGE, SOFT BOTTOM AND OYSTER SHELL HABITATS ALONG AN ESTUARINE SALINITY GRADIENT IN BARATARIA BAY, LOUISIANA

### **Introduction**

Spotted seatrout, *Cynoscion nebulosus*, are known to initially feed upon plankton, and then on immature shrimp and small fish species found in shallow vegetated habitats as they mature (Arnold et al. 1976). Adult spotted seatrout are known to be opportunistic carnivores (Lassuy 1983), and they are often referred to as generalist feeders (Darnell 1958; Tabb 1961; Llanso et al. 1998). Russell (2004), investigated the diet of spotted seatrout in Barataria Bay, LA, and found that diet was generally consistent among habitats (marsh edge, soft bottom and oyster shell) and salinity gradients (oligohaline, mesohaline, and polyhaline) sampled. However, the degree of overlap of ingested prey items was less at the marsh edge habitat as compared to the soft bottom and oyster shell habitats. Russell (2004) suggested that the similarity in diet among spotted seatrout was likely due to the ubiquitous distribution of prey items and the movement of spotted seatrout among available habitats, and throughout the estuary. This movement among habitats was supported by the fact that prey items associated with specific habitat types (e.g., *Gammarus* amphipods associated with the marsh edge) were often found in the stomachs of spotted seatrout collected from other habitat types.

The study by Russell (2004) was based upon gut content analysis (GCA), which has long been a standard practice to study the diets of fish (Hyslop 1980). However, GCA only provides information about feeding immediately prior to capture. Moreover, items found in the fish guts are often digested beyond identification and the contribution of soft-bodied prey to the diet can be underestimated (Hyslop 1980). This has led fisheries biologists to look for alternative methods to infer trophic linkages, including stable isotopes. Stable isotopes have proven to be

useful tracers of fish foraging histories and have been used to describe trophic relationships among organisms in a variety of aquatic ecosystems (Deegan and Garritt 1997; Vander Zanden et al. 1997; Fry et al. 1999b). Stable isotope ratios have also been used to identify changes in habitat use by estuarine fishes (Deegan et al. 1990; Thorrold et al. 1998; Litvin and Weinstein 2004), estimate the size at settlement of larval fish (Herzka and Holt 2000; Herzka and Holt 2001), trace migration patterns of juvenile shrimp and fish (Fry 1983; Hesslein et al. 1991; Fry et al. 1999a) and track diet shifts in fish as they grow (Renones et al. 2002; Cocheret de la Moriniere et al. 2003; Melville and Connolly 2003).

Stable isotopes can be used to trace fish foraging histories because animal tissues reflect the isotopic composition of their prey in a predictable manner (Peterson and Fry 1987). This is because stable isotopes are accumulated in tissues over substantial periods of time (Fry and Sherr 1984). Therefore, individuals with similar diets should have similar isotopic compositions (Peterson and Fry 1987) and individual fish that have specialized diets or utilize specific habitats can have large dietary and isotopic differences between individuals of the same species (Fry et al. 1999b). Moreover, greater isotopic diversity would be expected among fish utilizing diverse habitats (Fry 2002b).

The majority of diet studies using stable isotopes focus on  $\delta^{13}\text{C}$  Carbon (C),  $\delta^{15}\text{N}$  Nitrogen (N) and  $\delta^{34}\text{S}$  Sulfur (S).  $\delta^{13}\text{C}$  is most often used to determine the base of the food web (Deegan et al. 1990; Graham et al. 2001), while  $\delta^{15}\text{N}$  has been used in many studies to determine the trophic level of organisms (Vander Zanden et al. 1997; Fry et al. 1999b; Vander Zanden et al. 2000).  $\delta^{34}\text{S}$  has been shown to be a useful tool for differentiating organisms collected from varying salinity regions (Fry 2002a; Fry 2002b; Litvin and Weinstein 2004). Moreover, the inclusion of

multiple stable isotopes has been shown to increase the ability to resolve food web structure as compared to a single stable isotope approach (Peterson et al. 1985).

GCA can be compared to isotopic composition of the consumer by investigating the isotopic composition of prey items. This comparison is based on the premise that a known level of change, fractionation, in isotopic composition is expected when you move across trophic levels. The expected fractionation of stable isotopes between trophic levels is between 0 and 1‰ for  $\delta^{13}\text{C}$  (DeNiro and Epstein 1978; Peterson and Fry 1987) and 0.5‰ for  $\delta^{34}\text{S}$  (Peterson and Fry 1987). A commonly used value of 3.4‰ for  $\delta^{15}\text{N}$  fractionation can be found in the literature (Vander Zanden et al. 1997). However,  $\delta^{15}\text{N}$  fractionation values vary widely, with Peterson and Fry (1987) suggesting 3 to 5‰ and Deegan et al. (1990) suggesting 2 to 4 ‰.

A few studies have attempted to compare the short-term diet of fish with gut content analyses to the long-term feeding history of fish with stable isotopes. Guiguer et al. (2002) demonstrated that isotope analyses and gut contents yielded consistent results. However, a lack of agreement between isotope analyses from tissues and gut contents can occur, which may indicate that long-term and short-term diets are not the same (Fry 1981). This disagreement can be used to identify dietary switches in response to migratory and habitat differences (Fry 1981). A study combining stable isotopes and GCA by Grey et al. (2002) used a method analogous to ‘Russian dolls’ where they examined not only the muscle tissue of ferox brown trout, *Salmo trutta*, but the gut contents at each trophic level of prey as well. They concluded that this method provided complementary data to the stable isotope analysis and thus information on the longer term, assimilated diet.

There have been few studies examining the food web dynamics of spotted seatrout with stable isotopes in the northern Gulf of Mexico. Holt and McEachron (2001) presented a paper at

the 2001 Estuarine Research Federation Biennial Conference investigating habitat use by spotted seatrout in Texas estuaries. They found a significant difference in the isotopic composition of spotted seatrout collected in estuaries with and without seagrass; however, to my knowledge these data are not yet published. Despite the fact that spotted seatrout are one of the most highly sought recreational finfish species in Louisiana, and that estuaries in Louisiana are experiencing a great deal of habitat alteration, little is known about the habitat specific food web dynamics of this estuarine dependant species.

Given that habitats offering higher fish growth, reproduction, and survival potential are deemed essential, what makes these habitats so productive? One answer may be habitat-specific availability of resources. So an important question to ask is ‘does preferential habitat use coincide with changes in available food resources?’ One way to address this question is to determine whether individuals of the same species utilizing different habitats have similar diets or diets that differ by habitat. The objective of this study was to describe and identify essential fish habitat of spotted seatrout by learning more about the habitat specific food web dynamics of this species. To achieve this, first, the composition of  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  stable isotopes were compared among spotted seatrout collected from marsh edge, soft bottom and oyster shell habitats located along a salinity gradient in Barataria Bay, Louisiana, to determine if the habitat use and salinity preferences of spotted seatrout was coincident with utilization of resources. Second, the isotopic composition of spotted seatrout tissue and the isotopic composition of the gut contents were compared to determine if there was a match between short-term and long-term foraging of spotted seatrout. Lastly, spotted seatrout length and isotopic composition were examined to determine if  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  compositions of spotted seatrout were size specific.

## **Methods and Materials**

### Study Area

All spotted seatrout collections were made in Barataria Bay, part of the Barataria-Terrebonne Estuarine Basin (BTEB) in coastal Louisiana (Figure 2.1). The BTEB encompasses an area of approximately 16, 575 square kilometers within the Mississippi Deltaic Plain. The basin is bordered by the Mississippi River to the east, the East Atchafalaya Basin Levee and Atchafalaya River on the west and the Gulf of Mexico to the south. Three sites within Barataria Bay: Fisherman's Point (29°31'50"N 90°05'00"W), Manilla Village (29°25'74"N 89°59'20"W), and Grand Terre/Queen Bess (29°17'20"N 89°55'90"W/29°18'42"N 89°57'70"W) were sampled (Figure 2.1). The salinity at these sites ranged from oligohaline to mesohaline to polyhaline among Fisherman's Point, Manilla Village, and Grand Terre/Queen Bess. These sites were chosen because they represented a range in salinity, and each contained the three habitat types of interest: marsh edge, soft bottom (mud/sand) and oyster shell. Since the Grand Terre site did not have oyster shell habitat Queen Bess, a nearby location, was chosen to represent the oyster shell habitat for the polyhaline site. Although oyster shell density differed at the three sites sampled, the within site variability was the comparison of interest. Klein digital side-scan sonar was used in an earlier study to differentiate oyster shell bottom from soft bottom (mud/sand). The swath format of the side-scan sonar provides a two dimensional acoustic image of bottom hardness (reflectance), surface texture (roughness) and topography. Habitat specific sampling

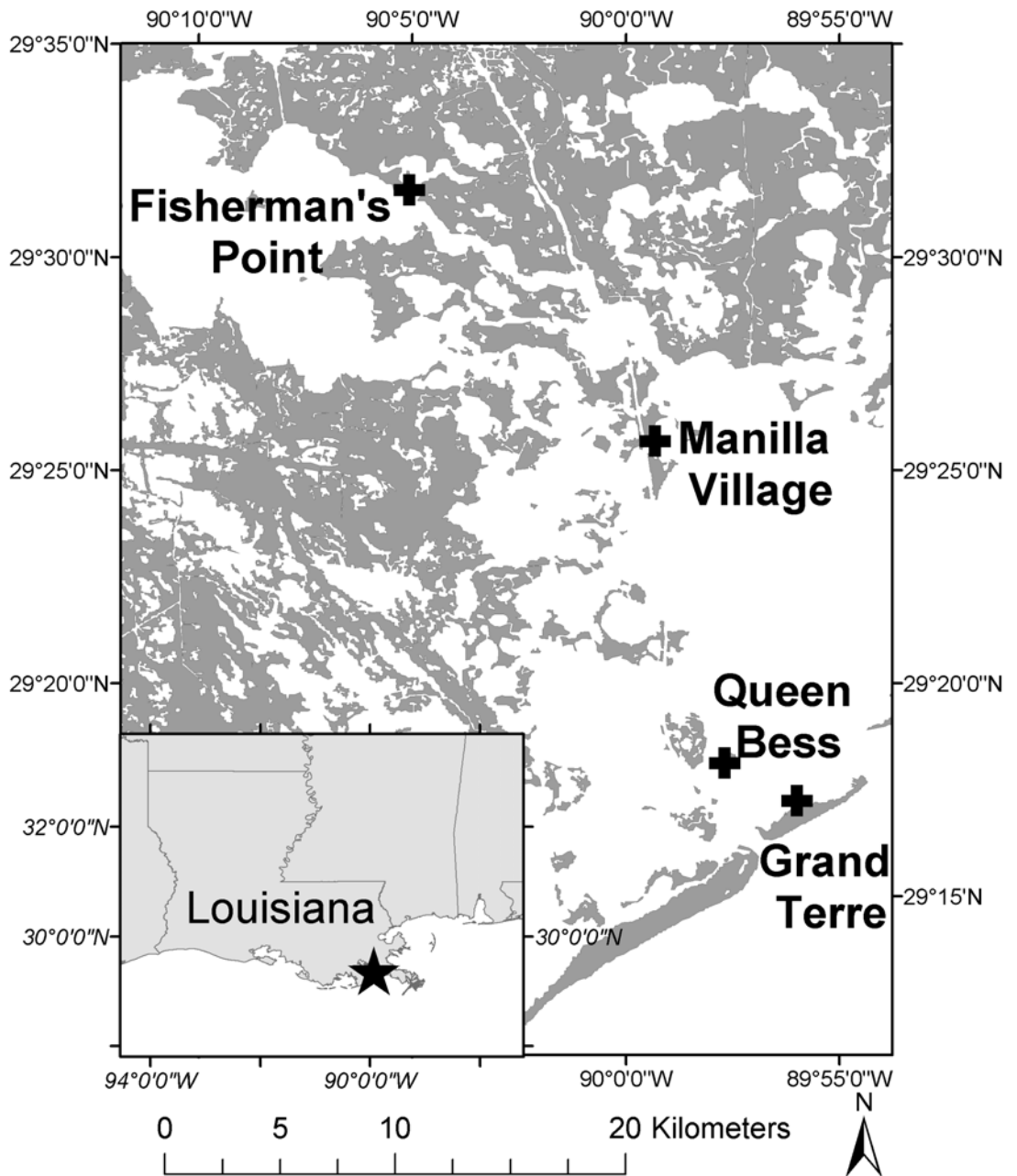


Figure 2.1. Map of Barataria Bay, Louisiana, and sampling sites: Grand Terre, Queen Bess, Manilla Village and Fisherman's Point.

locations were chosen based on these side-scan surveys (see Figures 1.2 to 1.5). In addition, SCUBA collections of bottom sediments were made to confirm the bottom type of habitats.

### Sampling Protocol

Monthly sampling began in May 2003 and was completed in May 2004, with the exception of December 2003, which was not sampled due to inclement weather. All spotted seatrout were collected with a 46.5 m x 2.48 m gill net at the soft bottom and oyster shell habitat, and a 46.5 m x 1.24 m gill net at the marsh edge habitat due to the shallower depth of the water at the marsh perimeter. All nets consisted of five 9.3 m panels, with the following bar mesh sizes: 1.27, 1.91, 2.54, 3.18 and 3.81 cm. One gill net was set per habitat type per site for one hour. Spotted seatrout were collected after one hour, and gill nets were then reset in the same place for another hour to replicate the sample in time. Spotted seatrout collected were put in an ice slurry with MS 222, then bagged and left on ice to be frozen later. In the laboratory, spotted seatrout were individually measured for standard length (SL) (cm), weighed (g) and a small piece of muscle tissue, about 1 x 1 cm, was taken just below the dorsal fin to be analyzed for isotopic composition. Muscle tissue samples were dried at 60°C for 24 hours in a DX 600 drying oven, and then ground with a Crescent Wig-L-Bug. Using a Precision XB Series balance, and then 4.0-5.0 mg of ground tissue of each individual was combined with approximately 10.0 mg of precombusted Vanadium pentoxide ( $V_2O_5$ ) and placed in an aluminum capsule. Prepared samples were then analyzed for the isotopic composition of  $\delta^{13}C$ ,  $\delta^{15}N$  and  $\delta^{34}S$  stable isotopes with a Finningan MAT DeltaPlus continuous-flow stable isotope mass spectrometer. All samples were analyzed in the laboratory of Dr. Brian Fry at the Coastal Ecology Institute, Louisiana State University.

The second portion of this study, which included analyzing the isotopic composition of prey contents collected from the spotted seatrout, used the gut content collections made by Micah Russell as part of his Masters thesis project (Russell 2004). This portion of the study was included part way through the project and therefore the gut contents of all spotted seatrout were not kept for analysis. The gut contents were however kept for 40 spotted seatrout, and the prey items of each spotted seatrout were separated into major taxonomic groups (e.g., fish, detritus, and zooplankton). The small amount of physical sample available for some of the prey categories made it unfeasible to run the analysis by individual prey category for each spotted seatrout. Therefore, it was decided to homogenize the different prey categories for multiple spotted seatrout, grouped by site and season. In total, 19 of these homogenized samples were analyzed for isotopic composition. Thus each sample was made up of gut contents from more than one spotted seatrout, although all seatrout in each sample were collected from the same site and season. The reasoning behind the homogenization of samples was that the isotopic composition values would be averaged in the end, so there was no reason not to go ahead and average them from the beginning. Prey contents, which had been previously dried by Russell (2004), once homogenized were then prepared for isotope analysis following the same methods detailed above.

Isotopic composition ratios are expressed in  $\delta$  notation, defined as the parts per thousand deviation from a standard material:

$$\delta^{13}\text{C}, \delta^{15}\text{N} \text{ or } \delta^{34}\text{S} = [((R_{\text{sample}}/R_{\text{standard}}) - 1) \times 1000]$$

where  $R = {}^{13}\text{C}/{}^{12}\text{C}$ ,  ${}^{15}\text{N}/{}^{14}\text{N}$  or  ${}^{34}\text{S}/{}^{32}\text{S}$ . The international standards PeeDee *Belemnitella americana* (PBD) for  $\delta^{13}\text{C}$ , atmospheric  $\text{N}_2$  for  $\delta^{15}\text{N}$  and Canyon Diablo Troilite (CDT) for  $\delta^{34}\text{S}$  were used in this study.

## Statistical Analyses

An analysis of variance (ANOVA) (SAS Institute 2002) was used to test whether the  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout differed among sites, habitats and in relation to standard length. Variables that were significant at the level of  $\alpha=0.05$  were further tested using the Tukey HSD post-ANOVA test to determine which variables accounted for the differences detected in the ANOVA. A total of 110 spotted seatrout were used in these analyses. Three outliers were removed from the  $\delta^{34}\text{S}$  isotopic composition data to achieve normality. These outliers were identified through examination of the residual by predicted values plot of  $\delta^{34}\text{S}$  samples by site in SAS (SAS Institute 2002). Due to time constraints and selection criteria of sampling sites treatments were not replicated and therefore caution should be used when extrapolating results to areas other than those sampled during this project (Hurlbert 1984).

An ANOVA (SAS Institute 2002) was used to test whether the  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout prey contents differed among sites. The variable habitat was not included in this analysis, because the small sample size required the homogenization of samples from different habitats. A Tukey HSD post-ANOVA test was used to determine which sites accounted for the differences detected in the ANOVA. As well, to test whether or not there was a match between short and long-term foraging of spotted seatrout among sites, mean  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic compositions of spotted seatrout were compared to mean  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic compositions of the prey.

Linear regression was employed to test the relationship between the  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout and standard length. Again, the three outliers were removed from the  $\delta^{34}\text{S}$  isotopic composition data.

## Results

### Isotopic Composition of Spotted Seatrout among Sites and Habitats

One hundred and ten spotted seatrout were analyzed for isotopic composition during this study. A total of 51 spotted seatrout were collected from the Grand Terre/Queen Bess site, 45 from Manilla Village and 14 from Fisherman's Point. By habitat, which included 23 collected near the marsh edge, 32 from soft bottom habitat and 55 from oyster shell. Spotted seatrout muscle tissue had a mean  $\delta^{13}\text{C}$  value of  $-20.73\text{‰}$ , and ranged from  $-23.39$  to  $-18.26\text{‰}$ , a mean  $\delta^{15}\text{N}$  value of  $13.68\text{‰}$ , and ranged from  $10.83$  to  $15.72\text{‰}$ , and a mean  $\delta^{34}\text{S}$  value of  $11.24\text{‰}$ , and ranged from  $8.78$  to  $13.45\text{‰}$ .

The mean  $\delta^{13}\text{C}$  value of spotted seatrout differed significantly among sites ( $p < 0.01$ , Table 2.1) with a mean value of  $-20.39\text{‰}$  ( $-22.17$  to  $-18.48\text{‰}$ ) at Grand Terre/Queen Bess,  $-20.86\text{‰}$  ( $-22.72$  to  $-18.26\text{‰}$ ) at Manilla Village and  $-21.55\text{‰}$  ( $-23.39$  to  $-18.72\text{‰}$ ) at Fisherman's Point. A Tukey HSD post-ANOVA test indicated that spotted seatrout collected at the oligohaline site, Fisherman's Point, had significantly lower  $\delta^{13}\text{C}$  isotopic compositions than those collected from the mesohaline, Manilla Village and polyhaline, Grand Terre/Queen Bess sites (Table 2.2, Figures 2.2 and 2.3).

The mean  $\delta^{15}\text{N}$  value of spotted seatrout also differed significantly among sites ( $p < 0.01$ , Table 2.3) with a mean of  $14.07\text{‰}$  ( $12.56$  to  $15.72\text{‰}$ ) at Grand Terre/ Queen Bess,  $13.44\text{‰}$  ( $11.09$  to  $14.66\text{‰}$ ) at Manilla Village and  $13.02\text{‰}$  ( $10.83$  to  $14.22\text{‰}$ ) at Fisherman's Point. A Tukey HSD post-ANOVA test indicated that the  $\delta^{15}\text{N}$  isotopic composition of spotted seatrout was significantly higher at the polyhaline site, Grand Terre/Queen Bess as compared to Manilla Village and Fisherman's Point (Table 2.4, Figure 2.2), However, there was also a significant site

by habitat interaction ( $p < 0.01$ , Tables 2.3 and 2.5), which indicated that the main effects were not consistent across all sites and habitats.

The mean  $\delta^{34}\text{S}$  value of spotted seatrout also differed significantly among sites ( $p < 0.01$ , Table 2.6), with a mean of 11.35‰ (10.08 to 13.19‰) at Grand Terre/Queen Bess, 11.29‰ (8.78 to 13.45‰) at Manilla Village and 10.70‰ (8.92 to 12.17‰) at Fisherman's Point. A Tukey HSD post-ANOVA test indicated that the  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout collected from Grand Terre/Queen Bess and Manilla Village, the polyhaline and mesohaline sites respectively, had significantly higher  $\delta^{34}\text{S}$  isotopic compositions than those collected from Fisherman's Point, the oligohaline site (Table 2.7, Figure 2.3).

The mean  $\delta^{13}\text{C}$  value of spotted seatrout differed significantly among habitats ( $p < 0.01$ , Table 2.1), with a mean of -20.15‰ (-22.72 to -18.26‰) at the marsh edge, -20.89‰ (-2.72 to -18.78‰) at the soft bottom habitat and -20.88‰ (-23.39 to -18.71‰) at the oyster shell habitat. A Tukey HSD post-ANOVA test indicated that the  $\delta^{13}\text{C}$  isotopic composition of spotted seatrout collected along the marsh edge was significantly higher than those collected over the soft bottom and oyster shell habitats (Table 2.2, Figures 2.4 and 2.5). There was no significant difference in the  $\delta^{15}\text{N}$  isotopic composition ( $p = 0.31$  Tables 2.3 and 2.4, Figure 2.4) among habitats although there was a significant site by habitat interaction, indicating that the main effects were inconsistent (Table 2.5). There was also no significant difference in  $\delta^{34}\text{S}$  isotopic composition ( $p = 0.07$ , Tables 2.6 and 2.7, Figure 2.5) of spotted seatrout collected among the different habitat types.

#### Isotopic Composition of Prey among Sites

A total of 40 spotted seatrout were analyzed for the isotopic composition of their prey contents during this study. The previously described combination of prey samples resulted in a

Table 2.1. Analysis of variance of  $\delta^{13}\text{C}$  isotopic composition for spotted seatrout collected in Barataria Bay, LA, between May 2003 and May 2004.

$\delta^{13}\text{C}$ Carbon	d.f.	F	MS	p-value
Site	2	8.97	8.06	< 0.01
Habitat	2	6.01	5.40	< 0.01
Standard length	1	8.4	7.55	< 0.01
Site x habitat	4	0.89	0.99	0.42

Table 2.2. Tukey HSD post-ANOVA test of the  $\delta^{13}\text{C}$  isotopic composition of spotted seatrout collected among sites and habitats. Different letters indicate a significant difference.

Tukey HSD	$\delta^{13}\text{C}$ Carbon Mean	StdErr	N	Site
A	-20.39	0.13	51	Grand Terre/Queen Bess
A	-20.86	0.15	45	Manilla Village
B	-21.55	0.33	14	Fisherman's Point
A	-20.15	0.24	23	Marsh edge
B	-20.89	0.19	32	Soft bottom
B	-20.88	0.13	55	Oyster shell

Table 2.3. Analysis of variance of  $\delta^{15}\text{N}$  isotopic composition of spotted seatrout collected in Barataria Bay, LA, between May 2003 and May 2004.

$\delta^{15}\text{Nitrogen}$	d.f.	F	MS	p-value
Site	2	10.66	5.04	< 0.01
Habitat	2	1.18	0.56	0.31
Standard length	1	5.0	2.36	0.03
Site x habitat	4	2.95	1.40	0.02

Table 2.4. Tukey HSD post-ANOVA test of the  $\delta^{15}\text{N}$  isotopic composition of spotted seatrout collected among sites and habitats. Different letters indicate a significant difference.

Tukey HSD	$\delta^{15}\text{Nitrogen}$	StdErr	N	Site
A	14.07	0.10	51	Grand Terre/Queen Bess
B	13.44	0.10	45	Manilla Village
B	13.02	0.26	14	Fisherman's Point
A	13.63	0.26	23	Marsh edge
A	13.72	0.10	32	Soft bottom
A	13.68	0.10	55	Oyster shell

Table 2.5. Results from Tukey HSD post-2 way ANOVA test of effects comparing the  $\delta^{15}\text{N}$  isotopic composition of spotted seatrout collected among sites and habitats. Different letters indicate a significant difference.

SL	Marsh edge	Soft bottom	Oyster shell
Grand Terre/Queen Bess	14.22±0.20 A	13.94±0.16 A	13.98±0.20 A
Manilla Village	13.58±0.33 AB	13.42±0.23 AB	13.48±0.12 AB
Fisherman's Point	12.26±0.31 B	13.67±0.35 AB	13.42±0.23AB

Table 2.6. Analysis of variance of  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout collected in Barataria Bay, LA, between May 2003 and May 2004.

$\delta^{34}\text{Sulfur}$	d.f.	F	MS	p-value
Site	2	7.02	4.14	< 0.01
Habitat	2	2.69	1.59	0.07
Standard length	1	7.62	4.49	< 0.01
Site x habitat	4	1.24	0.73	0.30

Table 2.7. Tukey HSD post-ANOVA test of the  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout collected among sites and habitats. Different letters indicate a significant difference.

Tukey HSD	$\delta^{34}\text{Sulfur}$	StdErr	N	Site
A	11.35	0.12	50	Grand Terre/Queen Bess
A	11.29	0.21	43	Manilla Village
B	10.69	0.25	14	Fisherman's Point
A	11.47	0.29	21	Marsh edge
A	11.07	0.14	32	Soft bottom
A	11.25	0.16	54	Oyster shell

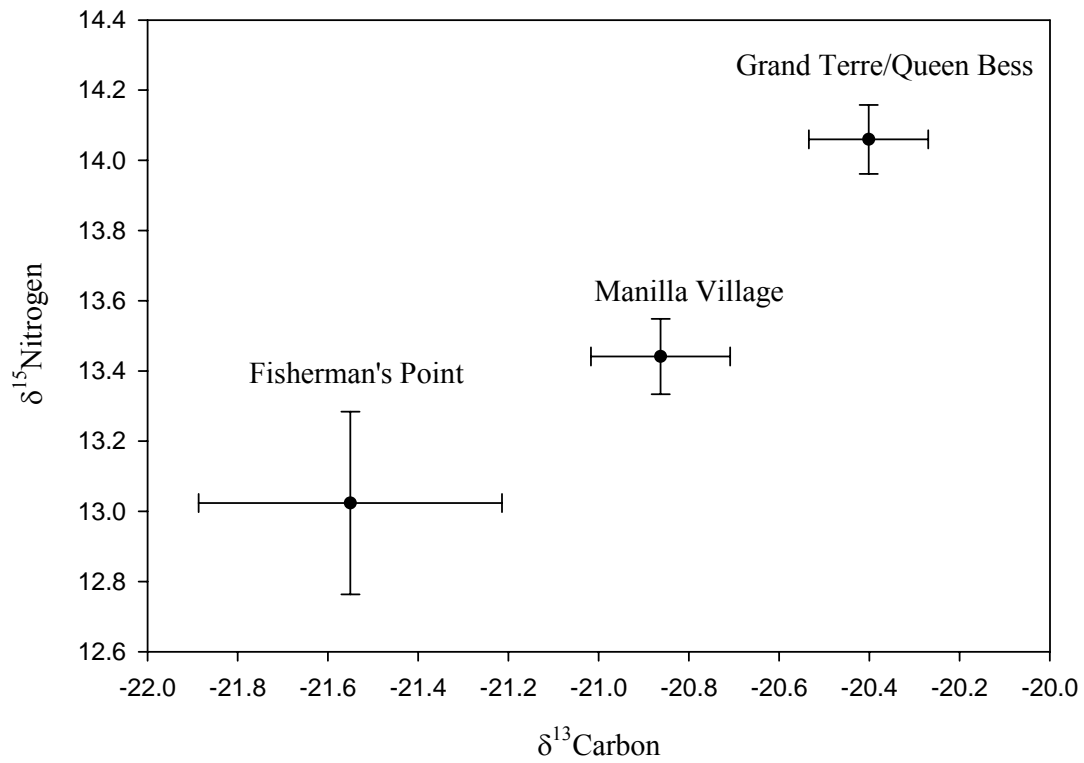


Figure 2.2. Carbon and nitrogen isotopic composition (mean  $\pm$  SE) of spotted seatrout for each site sampled in Barataria Bay, LA.

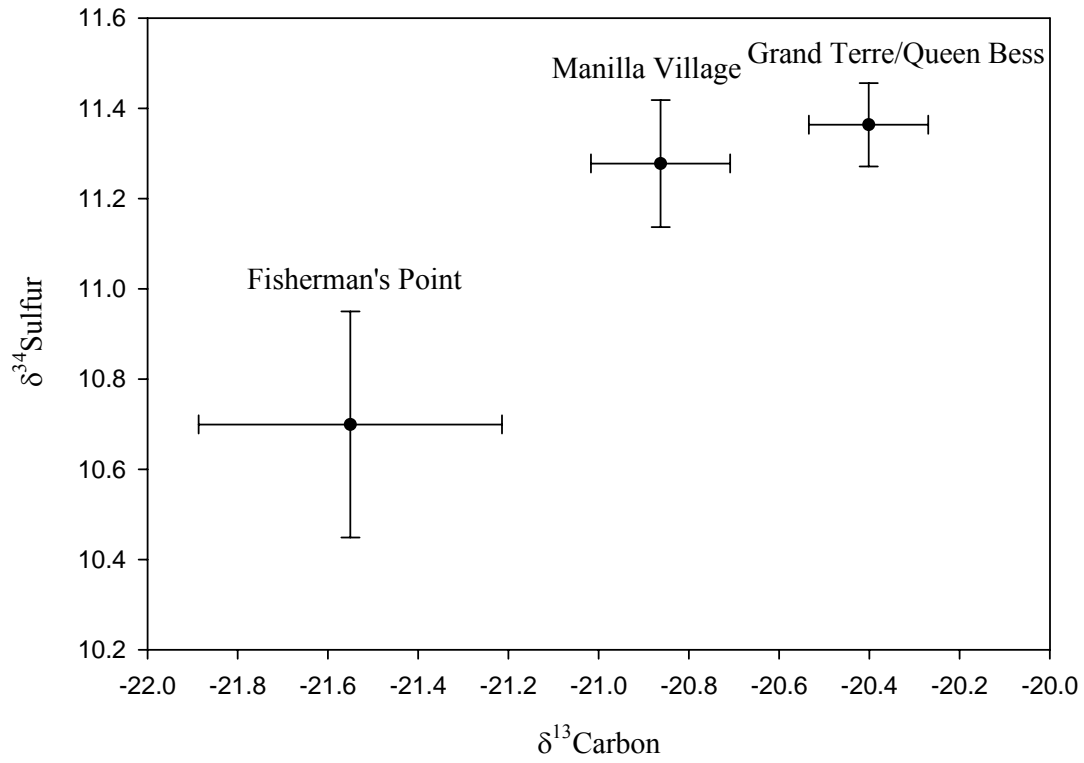


Figure 2.3. Carbon and sulfur isotopic composition (mean  $\pm$  SE) of spotted seatrout for each site sampled in Barataria Bay, LA.

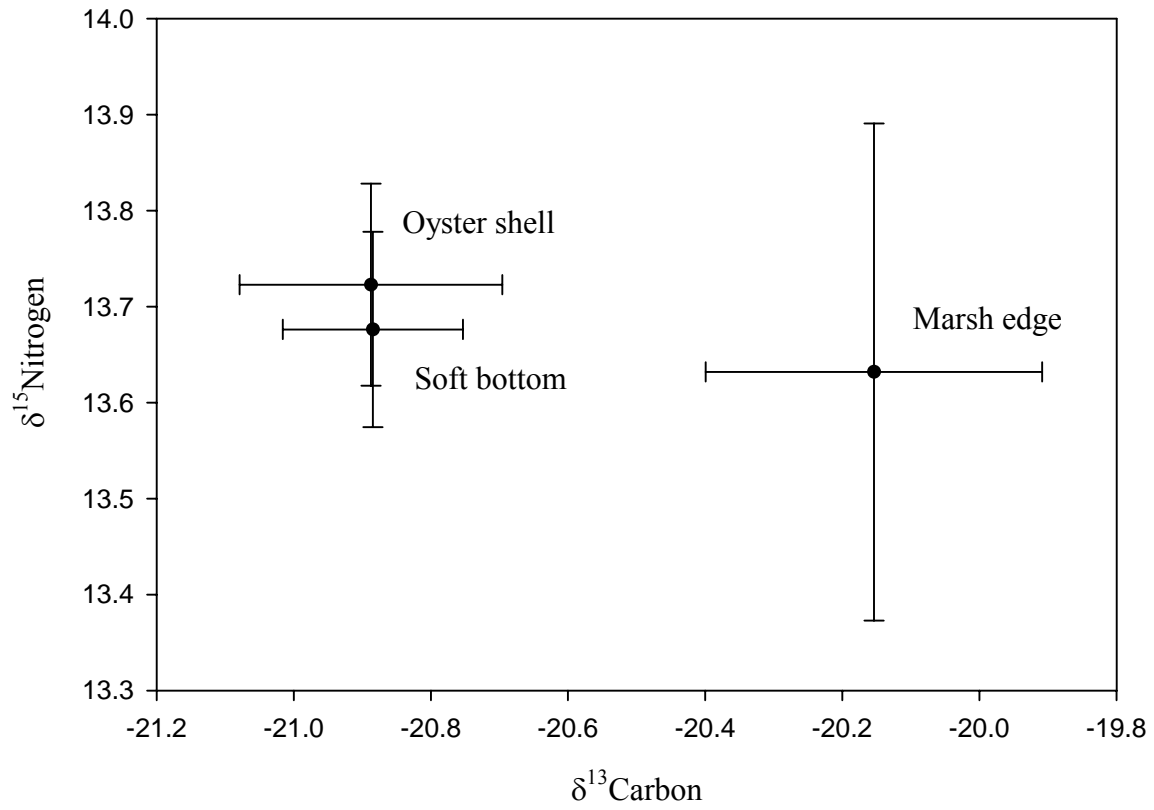


Figure 2.4. Carbon and nitrogen isotopic composition (mean  $\pm$  SE) of spotted seatrout for each habitat sampled in Barataria Bay, LA.

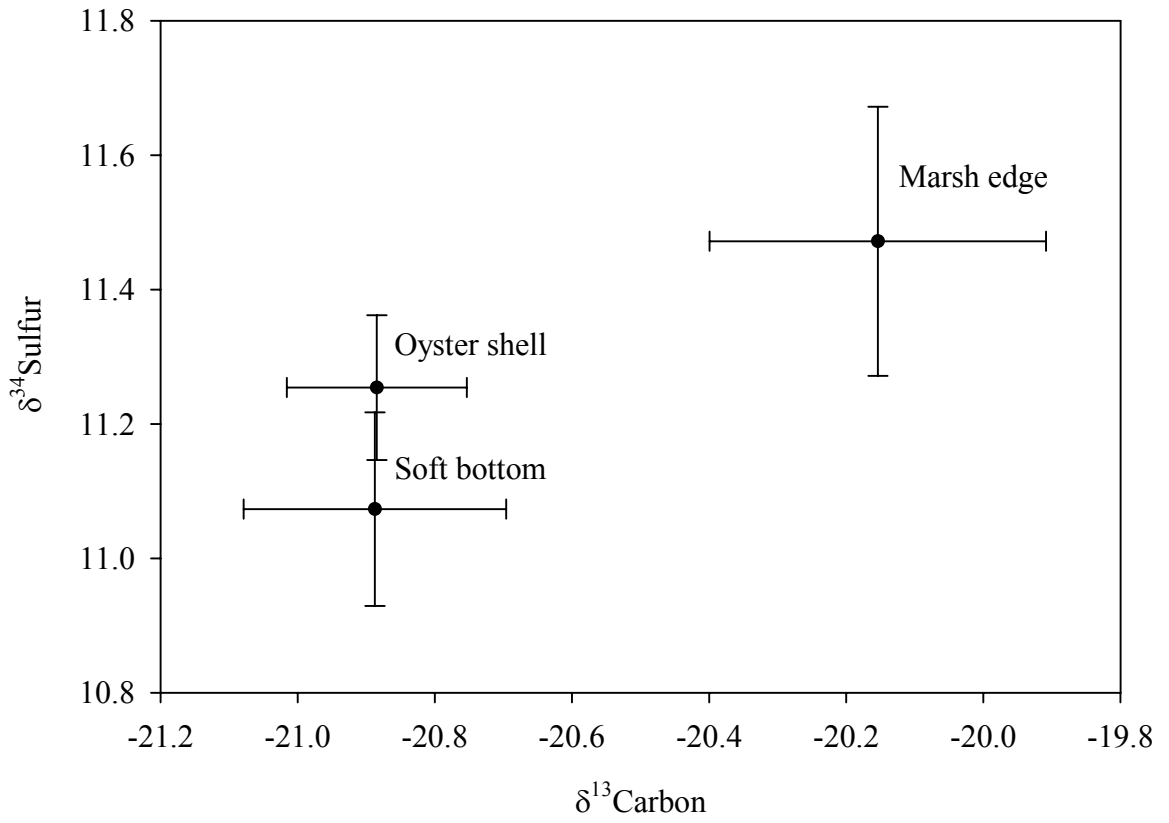


Figure 2.5. Carbon and sulfur isotopic composition (mean  $\pm$  SE) of spotted seatrout for each habitat sampled in Barataria Bay, LA.

total of 19 samples, representing 8 samples from Grand Terre/Queen Bess (based on 17 spotted seatrout), 6 from Manilla Village (based on 16 spotted seatrout) and 5 from Fisherman's Point (based on 7 spotted seatrout). The spotted seatrout prey contents had an overall mean of -21.82‰ for  $\delta^{13}\text{C}$ , ranging from -26.07 to -18.93‰, 10.68‰ for  $\delta^{15}\text{N}$ , ranging from 8.43 to 14.14‰ and 12.24‰ for  $\delta^{34}\text{S}$ , ranging from 8.05 to 15.8‰.

The mean  $\delta^{13}\text{C}$  value of spotted seatrout prey contents differed significantly among sites ( $p = 0.02$ , Table 2.8) with a mean of -20.49‰ (-21.28 to -18.93‰) at Grand Terre/ Queen Bess, -22.67‰ (-24.53 to -20.24‰) at Manilla Village and -22.92‰ (-26.07 to -20.49‰) at Fisherman's Point. In general, enrichment of  $\delta^{13}\text{C}$  was observed from the oligohaline site to the polyhaline site. A Tukey HSD post-ANOVA test indicated that prey contents from spotted seatrout collected at the oligohaline site, Fisherman's Point, had significantly lower  $\delta^{13}\text{C}$  isotopic compositions than those collected from the highest salinity site Grand Terre/Queen Bess. Manilla Village, the mesohaline sites did not differ significantly from either site (Table 2.9, Figures 2.6 and 2.7). Comparison of the isotopic composition of the spotted seatrout muscle tissue and the prey contents detected an enrichment of  $\delta^{13}\text{C}$  in spotted seatrout. Enrichment values of 0.10‰, 1.18‰ and 1.37‰ of spotted seatrout were found at Grand Terre/Queen Bess, Manilla Village and Fisherman's Point respectively (Table 2.12).

The mean  $\delta^{15}\text{N}$  value of spotted seatrout prey contents did not differ significantly among sites ( $p = 0.11$ , Tables 2.8 and 2.10), although a general enrichment of  $\delta^{15}\text{N}$  was detected from the oligohaline site, Fisherman's Point, to the polyhaline site, Grand Terre/Queen Bess (Figure 2.6). Mean values were 11.42‰ (9.40 to 14.14‰) at Grand Terre/Queen Bess, 10.54‰ (9.34 to 11.83‰) at Manilla Village and 9.66‰ (8.43 to 11.99‰) at Fisherman's Point. Comparison of the isotopic composition of the spotted seatrout tissue detected an enrichment of  $\delta^{15}\text{N}$  in the

spotted seatrout. Enrichment values of 2.65‰, 2.90‰ and 3.36‰ were found at Grand Terre/Queen Bess, Manilla Village and Fisherman's Point, respectively (Table 2.12).

The mean  $\delta^{34}\text{S}$  value of spotted seatrout prey contents differed significantly among sites ( $p < 0.01$ , Table 2.8) with a mean of 13.84‰ (11.71 to 15.80‰) at Grand Terre/Queen Bess, 10.87‰ (8.99 to 12.96‰) at Manilla Village and 11.32‰ (8.05 to 13.88‰) at Fisherman's Point. A Tukey's HSD post-ANOVA test indicated that spotted seatrout prey contents from the polyhaline site, Grand Terre/Queen Bess, had significantly higher  $\delta^{34}\text{S}$  isotopic compositions than those collected from both Manilla Village and Fisherman's Point, the mesohaline and oligohaline sites respectively (Table 2.11, Figure 2.7). Comparison of the isotopic composition of the spotted seatrout muscle tissue and the prey contents detected a depletion of  $\delta^{34}\text{S}$  in the spotted seatrout, at two of the three sites. Depletion values of -2.49‰, and -0.62‰ were found at Grand Terre/Queen Bess and Fisherman's Point respectively, while an enrichment value of 0.42‰ was found at Manilla Village (Table 2.12).

#### Standard Length and Isotope Relationships

Standard length of spotted seatrout was significantly related to the  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic composition of their muscle tissue (Tables 2.1, 2.3 and 2.6). While the  $\delta^{13}\text{C}$  isotopic composition of spotted seatrout generally decreased as standard length increased, this relationship was not significant ( $N = 110$ ,  $R^2 = 0.03$ ,  $F = 3.04$ ,  $p = 0.08$ , Figures 2.8). The  $\delta^{15}\text{N}$  isotopic composition of spotted seatrout significantly increased as standard length increased, ( $N = 110$ ,  $R^2 = 0.16$ ,  $F = 20.39$ ,  $p < 0.01$ , Figure 2.9), while the  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout significantly decreased as standard length increased ( $N = 107$ ,  $R^2 = 0.05$ ,  $F = 5.88$ ,  $p = 0.02$ , Figures 2.10).

Table 2.8. Analysis of variance of  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout prey contents by site collected in Barataria Bay, LA, between May 2003 and May 2004.

	MS	F	d.f.	p-value
$\delta^{13}\text{Carbon}$	12.24	5.05	2	0.02
$\delta^{15}\text{Nitrogen}$	4.85	2.52	2	0.11
$\delta^{34}\text{Sulfur}$	18.01	6.63	2	<0.01

Table 2.9. Tukey HSD post-ANOVA test of the  $\delta^{13}\text{C}$  isotopic composition of spotted seatrout prey contents collected among sites. Different letters indicate a significant difference.

Tukey HSD	$\delta^{13}\text{Carbon}$	N	Site
A	-20.49	8	Grand Terre/Queen Bess
AB	-22.67	6	Manilla Village
B	-22.92	5	Fisherman's Point

Table 2.10. Tukey HSD post-ANOVA test of the  $\delta^{15}\text{N}$  isotopic composition of spotted seatrout prey contents collected among sites. Different letters indicate a significant difference.

Tukey HSD	$\delta^{15}\text{Nitrogen}$	N	Site
A	11.42	8	Grand Terre/Queen Bess
A	10.54	6	Manilla Village
A	9.66	5	Fisherman's Point

Table 2.11. Tukey HSD post-ANOVA test of the  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout prey contents collected among sites. Different letters indicate a significant difference.

Tukey HSD	$\delta^{34}\text{S}$ Sulfur	N	Site
A	13.84	8	Grand Terre/Queen Bess
B	10.87	6	Manilla Village
B	11.32	5	Fisherman's Point

Table 2.12. Mean  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  isotopic compositions of spotted seatrout muscle tissue and prey contents by site.

	GT/QB	MV	FP	GT/QB	MV	FP	GT/QB	MV	FP
	$\delta^{13}\text{C}$	$\delta^{13}\text{C}$	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$	$\delta^{15}\text{N}$	$\delta^{15}\text{N}$	$\delta^{34}\text{S}$	$\delta^{34}\text{S}$	$\delta^{34}\text{S}$
Tissue	-20.39	-20.86	-21.55	14.07	13.44	13.02	11.35	11.29	10.7
Prey	-20.49	-22.67	-22.92	11.42	10.54	9.66	13.84	10.87	11.32
Difference	0.10	1.81	1.37	2.65	2.90	3.36	-2.49	0.42	-0.62

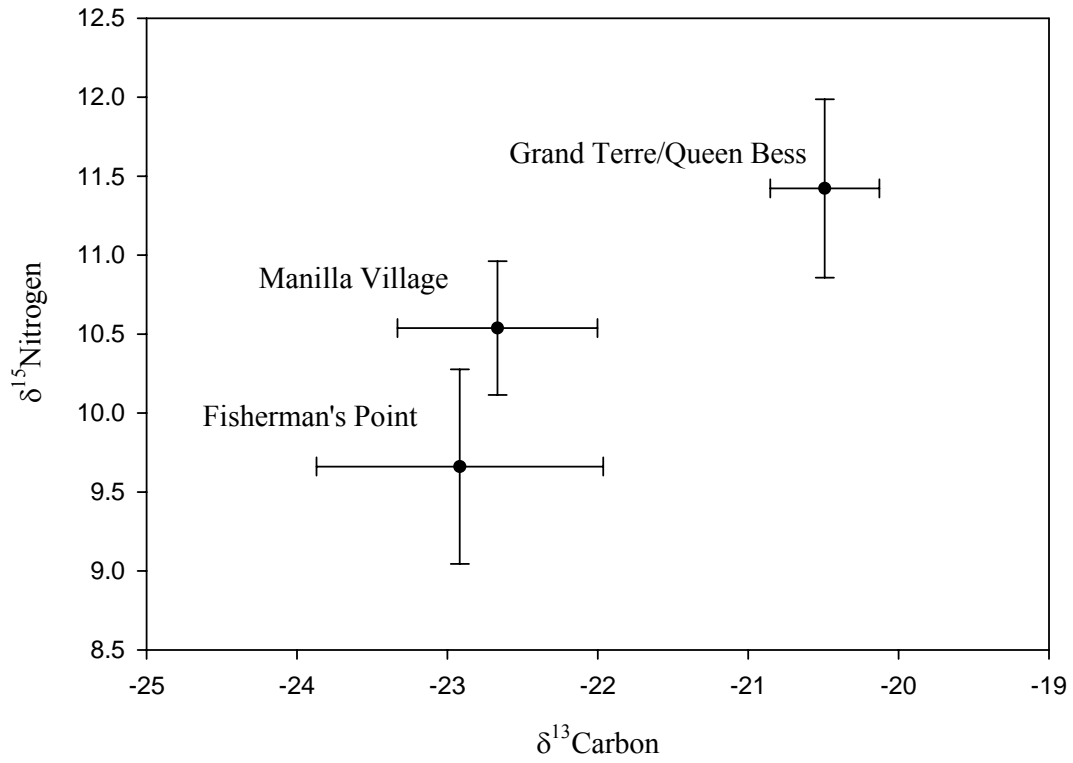


Figure 2.6. Carbon and nitrogen isotopic composition (mean  $\pm$  SE) of spotted seatrout prey for each site sampled in Barataria Bay, LA.

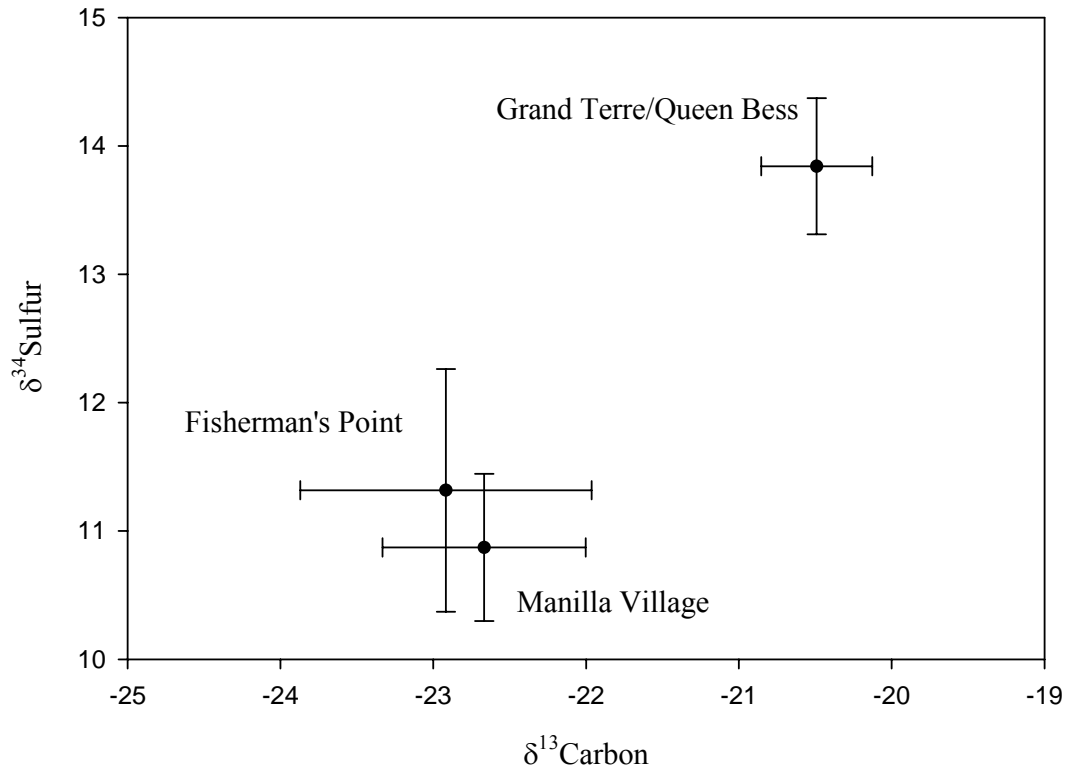


Figure 2.7. Carbon and sulfur isotopic composition (mean  $\pm$  SE) of spotted seatrout prey for each site sampled in Barataria Bay, LA.

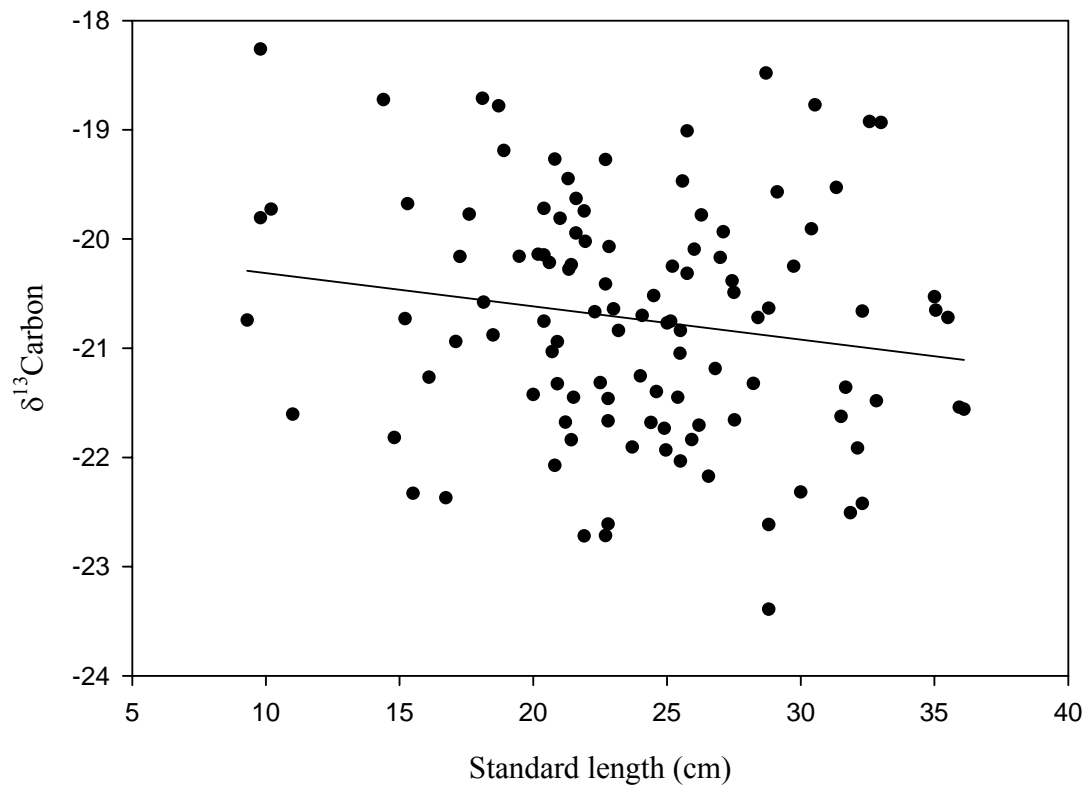


Figure 2.8. Relationship between standard length and the carbon isotopic composition of spotted seatrout. Symbols represent individuals.

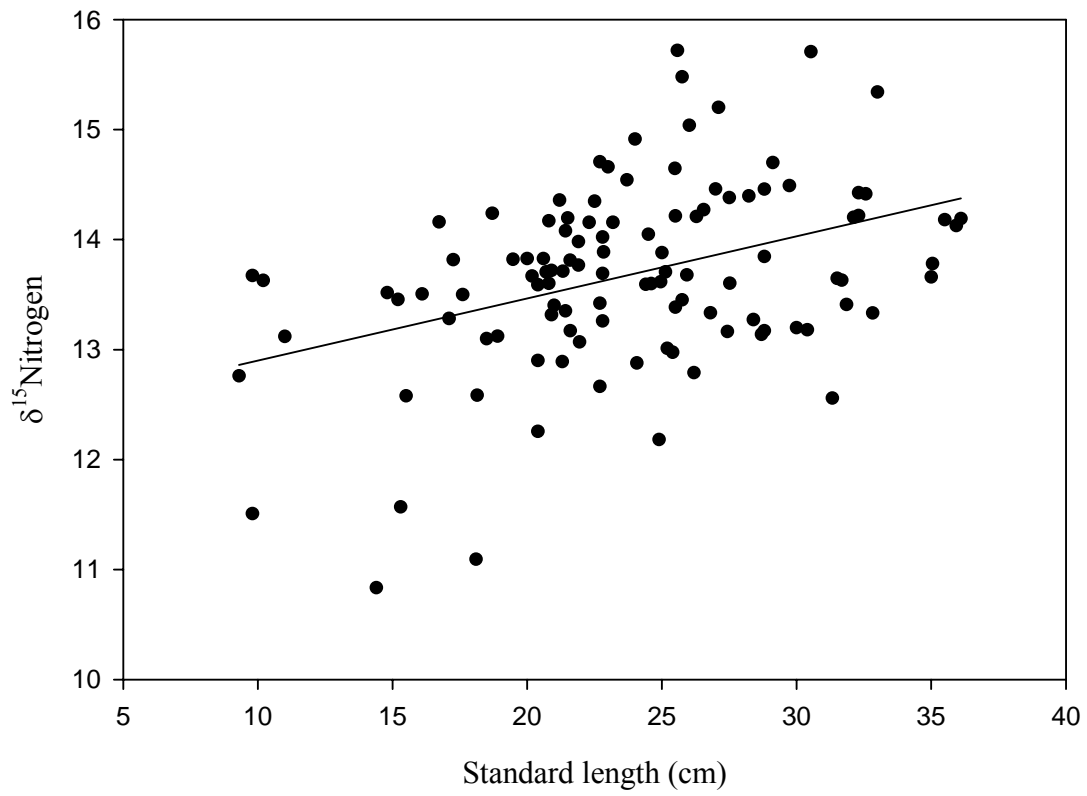


Figure 2.9. Relationship between standard length and the nitrogen isotopic composition of spotted seatrout. Symbols represent individuals.

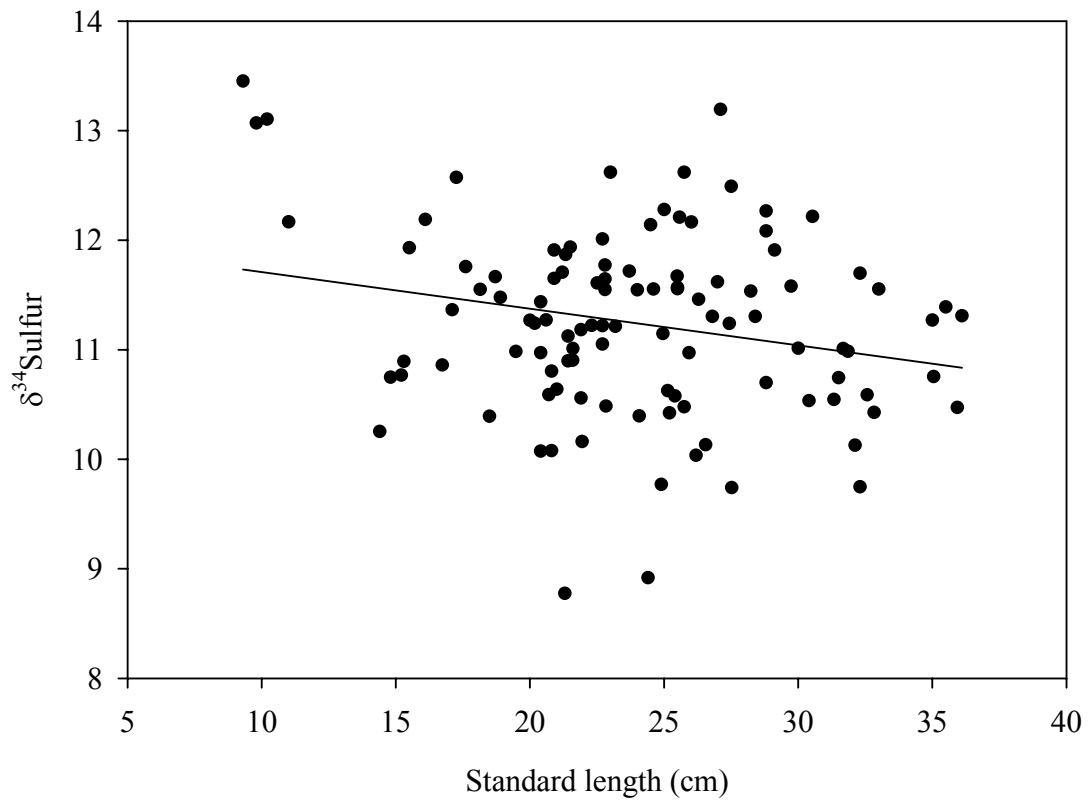


Figure 2.10. Relationship between standard length and the sulfur isotope composition of spotted seatrout. Symbols represent individuals.

## Discussion

Spatial variability in the water geochemistry along salinity gradients in estuaries can be detected using stable isotopes as tracers (Fry 2002a). In this study, the stable isotopic composition of spotted seatrout collected in Barataria Bay, LA, differed among sites located along a salinity gradient.

Enrichment of  $\delta^{13}\text{C}$  in spotted seatrout at the highest salinity site with declining  $\delta^{13}\text{C}$  at the lower salinity sites is consistent with some degree of site fidelity as opposed to large-scale movement between salinity zones in the bay (Fry 2002a,b). Enrichment of  $\delta^{13}\text{C}$  in higher salinities likely reflects differences in the source of carbon at the base of the food web, with an atmospheric carbon dioxide source in fresher waters compared to a bicarbonate source in the well-buffered marine waters (Peterson and Fry 1987).

Although a depletion of  $\delta^{15}\text{N}$  would be expected in fish collected from fresher waters as compared to marine waters (Fry 2002a; Fry 2002b), a trend of  $\delta^{15}\text{N}$  enrichment with increasing salinity was detected during this study. Barataria Bay is considered an inverse or offshore estuary that is heavily influenced by the nutrient rich waters of the Mississippi River entering the estuary through the passes rather than from the bays headwaters. This enrichment likely explains the unusual patterns of  $\delta^{15}\text{N}$  observed in Barataria Bay spotted seatrout (personal communication B. Fry, CEI, LSU).

Higher  $\delta^{34}\text{S}$  isotopic composition of spotted seatrout from the mid and high salinity sites as compared to the low salinity site is most likely attributable to the presence of marine sulfates in the higher salinity waters (Peterson and Fry 1987; Fry 2002a). Other investigators found that fish collected along a salinity gradient have enriched  $\delta^{34}\text{S}$  isotopic compositions in regions of higher salinity (Deegan and Garritt 1997; Fry 2002b). This enrichment may be a reflection of

differences in the base of the food web, which may indicate a greater importance of marine phytoplankton at the high salinity site, as compared to a greater importance of *Spartina* sp. or upland plants at the lower salinity sites, given that  $\delta^{34}\text{S}$  becomes more depleted from marine phytoplankton to upland plants to *Spartina* sp. (Peterson and Fry, 1987).

Variability in stable isotopes has also been used to detect differences in habitat use of fishes in estuaries (Deegan and Garritt 1997; Fry 2002b; Litvin and Weinstein 2004). The enrichment of  $\delta^{13}\text{C}$  in spotted seatrout collected along the marsh edge may be attributable to a greater influence of either *Spartina* sp. or benthic microalgae as a carbon source in the diet of those spotted seatrout, as both *Spartina* sp. and benthic microalgae are enriched in  $\delta^{13}\text{C}$  (-13 and -17‰, respectively) relative to phytoplankton (-21‰) (Peterson and Fry 1987; Deegan and Garritt 1997). In contrast, phytoplankton may be a more important source of carbon to spotted seatrout collected over the soft bottom and oyster shell habitats. This difference among habitats may be attributable to the fact that spotted seatrout were on average smaller along the marsh edge than those collected over soft bottom and oyster shell habitats (see Chapter 1).

Similar to the results found for the spotted seatrout muscle tissue, the stable isotopic composition of the prey suggests an enrichment of  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  along the freshwater to marine gradient. Thus while Russell (2004) found no significant difference in the prey contents of spotted seatrout among sites, these prey items may also have been spending more time in the region where they were consumed.

Comparison of the  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  isotopic composition of the spotted seatrout and their prey contents suggests that the prey contents fell about one trophic level below spotted seatrout, given that fractionation is normally between 0 and 1‰ between trophic levels for  $\delta^{13}\text{C}$  (DeNiro and Epstein 1978; Peterson and Fry 1987) and 3.4‰ for  $\delta^{15}\text{N}$  (Vander Zanden et al. 1997). These

results are consistent with the diet study of Russell (2004) who found that spotted seatrout in Baratavia Bay mainly consumed small-bodied fish (e.g., Gulf menhaden, *Brevoortia patronus* and threadfin shad, *Alosa chrysochloris*), which are both one trophic level below spotted seatrout.

The  $\delta^{34}\text{S}$  isotopic composition of the prey contents at Manilla Village and Fisherman's Point fell close to the expected difference of 0.5‰ per trophic level (Peterson and Fry 1987), although a depletion rather than enrichment was found at Fisherman's Point. In contrast, comparison of the  $\delta^{34}\text{S}$  isotopic composition of the spotted seatrout and prey contents at Grand Terre/Queen Bess indicated spotted seatrout were depleted in  $\delta^{34}\text{S}$  as compared to the prey. The enriched  $\delta^{34}\text{S}$  values found in the prey contents of spotted seatrout collected from the Grand Terre/Queen Bess site may 1) be attributable to the high amounts of sulfates in this region, 2) indicate that spotted seatrout had been feeding even further offshore just prior to capture, 3) suggest that prey at the Grand Terre/Queen Bess site are distinct from the other two sites, 4) be a reflection of the small sample size of the prey as compared to the relatively large sample size of spotted seatrout muscle tissue; or 5) indicate that short and long-term foraging of spotted seatrout differ. Although, none or a combination of all of these hypotheses may be influencing the  $\delta^{34}\text{S}$  values found in the prey contents of spotted seatrout collected from the Grand Terre/Queen Bess.

Given that rapidly growing animals can quickly reflect the isotopic composition of their prey (Fry and Arnold 1982), the relationship between spotted seatrout length and isotopic composition was explored. This study revealed a general depletion of  $\delta^{13}\text{C}$  with length of spotted seatrout. However, the relationship between  $\delta^{13}\text{C}$  and the standard length of fish is unclear. Renones et al. (2002) and Cocheret de la Moriniere et al. (2003) found no relationship between the  $\delta^{13}\text{C}$  isotopic composition and length of dusky grouper, *Epinephalus marginatus*, from the

Mediterranean and coral reef fish from the Netherlands Antilles, respectively. However, Herzka and Holt (2000) found a significant relationship between  $\delta^{13}\text{C}$  fractionation and the standard length of larval red drum, where fractionation decreased as length increased. This significant relationship was associated with a change in diet attributable to a change from pelagic to demersal habitat following larval settlement. Herzka et al. (2001) further used this isotopic change to create a model to estimate size at settlement.

A clear relationship between  $\delta^{15}\text{N}$  and fish length is expected, as  $\delta^{15}\text{N}$  has been used in many studies to determine the trophic level of organisms (Vander Zanden et al. 1997; Fry et al. 1999b; Vander Zanden et al. 2000). Studies including Renones et al. (2002), Cocheret de la Moriniere et al. (2003) and Melville and Connolly (2003) found a significant relationship between fish length and  $\delta^{15}\text{N}$ , with  $\delta^{15}\text{N}$  increasing with length. In this study of spotted seatrout,  $\delta^{15}\text{N}$  also generally increased as standard length increased. Had more juvenile and young-of-the-year been collected, evidence of an ontogenetic shift from pelagic to demersal habitat may have been detected and strengthened this relationship. However, Herzka and Holt (2000), who did detect an ontogenetic shift in red drum, found no significant relationship between fish length and  $\delta^{15}\text{N}$ .

The relationship between  $\delta^{34}\text{S}$  and fish length has not been explored, to my knowledge, in the literature. In this study,  $\delta^{34}\text{S}$  significantly increased as standard length increased. Given that a change in  $\delta^{34}\text{S}$  can be expected with depth (Peterson and Fry 1987), it is possible that this relationship may be attributable to smaller spotted seatrout that had been feeding in the pelagic zone pre-settlement. These pre-settlement fish would likely differ in  $\delta^{34}\text{S}$  as compared to larger spotted seatrout feeding in the benthos if tissue turnover rate were slow enough. However, because we did not collect any pre-settlement sized spotted seatrout this cannot be confirmed.

I conclude that individual spotted seatrout may not move widely throughout Barataria Bay, rather they exhibit some site fidelity with preference for salinity zones within the bay, although salinity preference appears to be on an individual fish level. These results are similar to those of Litvin and Weinstein (2004) who suggest that tidal action and/or individual fish movement was responsible for the observed differences in the isotopic compositions of fish collected along a salinity gradient in Delaware Bay. This inference of regional habitat use is supported by the isotopic composition of the prey contents, which also reflected a similar pattern among sites along the oligohaline to polyhaline gradient. Results also suggest that spotted seatrout exhibit some fidelity to habitat type whereby some individuals are spending more time along the marsh edge habitat as compared to soft bottom and oyster shell habitats. This trend highlights the importance of the marsh edge habitat to spotted seatrout, however this relationship may be a function of spotted seatrout size. This study suggests that conclusions drawn about habitat use by spotted seatrout based solely on gut contents may not provide the full scope of relative habitat value within Barataria Bay, LA.

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## CHAPTER 3: FISH ASSEMBLAGE STRUCTURE AMONG MARSH EDGE, SOFT BOTTOM AND OYSTER SHELL HABITATS ALONG AN ESTUARINE SALINITY GRADIENT IN BARATARIA BAY, LOUISIANA

### **Introduction**

In 2005, commercial fisheries landings in Louisiana exceeded 1 billion pounds and 247 million dollars, which accounted for about 26% of the total catch by weight in the lower 48 states (USDOC 2005). Additionally, recreational fishing in Louisiana can annually accounts for between \$703 million (USDI 2001) and \$1.2 billion (Gentner et al. 2001). Many of these commercial and recreationally important species are dependant on estuaries as nurseries, and for reproduction, food production and migrations at some point in their life history (Nelson et al. 2002). Despite the importance of estuaries to Louisiana's fisheries, they have been altered dramatically in recent years due to a number of anthropogenic and natural processes (Gosselink 1984; Turner 1997), and Louisiana currently accounts for about 80-90% of the total marsh loss in the continental United States. More specifically, the Barataria-Terrebonne Basin currently accounts for about 60% of land loss in Louisiana and is expected to account for about 80% by 2050 (Barras et al. 1994). This loss of habitat may be particularly detrimental to many fishes and macroinvertebrates that rely on salt marshes at some point in their life history (Rakocinski et al. 1992; Baltz et al. 1993; Peterson and Turner 1994). Given that this loss of fisheries habitat affects both species of commercial and recreational importance as well as the whole fish assemblage, there is no doubt a need to learn more about habitat specific associations in this altered environment.

Estuaries have a variety of habitats that exist in a mosaic, providing a complex environment for associated mobile species (Bell et al. 1991). Posey et al. (2000) emphasize that habitat types are not isolated units, but interconnected and should be managed as such. Despite

this, the density of fish often varies among habitat types, and detecting these differences can provide useful information on relative value (Baltz et al. 1993; Minello 1999). Numerous studies have shown that the density of fish differs between habitat types, and many of these habitat comparison studies have focused on vegetated versus non-vegetated habitats (Crowder and Cooper 1982; Orth et al. 1984; Pollard 1984; Zimmerman et al. 1984; Baltz et al. 1993; Irlandi and Crawford 1997; Rozas and Zimmerman 2000).

Three habitat types are predominant in Louisiana estuaries: marsh, soft bottom (mud/sand) and oyster shell. The value of marshes (Boesch and Turner 1984; Peterson and Turner 1994) and oyster reef/shell habitat (Zimmerman et al. 1989; Coen et al. 1999; Harding and Mann 1999) as nursery, feeding and breeding habitat for fishes is well recognized. However, the relative value of these habitats and how they compare to each other and soft bottom habitat is largely unknown. Minello (1999) points out that habitat specific use has not been comprehensively defined for many estuarine species.

Marsh and marsh edge have been shown to be important habitats to fisheries in the northern Gulf of Mexico, acting as an important nursery and refugia habitat for many fish species (Boesch and Turner 1984; Minello 1999; Zimmerman et al. 2000; Minello and Rozas 2002). Boesch and Turner (1984) found that marsh edge provides an abundance of food and refuge important for many fish species at some point in their life history. These properties of marsh edge habitats have putatively led to enhanced yields of some fish species, inferring evidence of a link between the nursery function of marshes and future yields of fisheries. Therefore, loss of this habitat could be detrimental to the survival of many fish species (Weinstein 1979; Zimmerman et al. 1984; Baltz et al. 1993; Peterson and Turner 1994).

Complex sub-tidal habitats such as those created by shell have also been shown to provide both substrate and refugia to juvenile fishes (Shulman 1985; Jordan et al. 1996). Sub-tidal shell habitats support a diverse community of polychaetes, crustaceans, bryozoans, hydroids, sponges and tunicates (Ruppert and Fox 1988). Moreover, oyster reef communities of fish and macro-invertebrates along the Atlantic and Gulf of Mexico coasts are highly diverse and include numerous species that are absent or found rarely in adjacent soft bottom habitats (see Coen et al. 1999). While Lehnert and Allen (2002) found that tray catches of fish were significantly greater in the sub-tidal oyster shell bottom than the inter-tidal oyster reef, and that shelly rubble bottoms supported a more diverse and abundant demersal fish assemblage than adjacent sandy or muddy sub-tidal creek bottom, few studies have focused on the importance of oyster shell habitat and how it compares to adjacent soft bottom habitats (Coen et al. 1999; Harding and Mann 2001). Moreover, even fewer studies have contemporaneously compared oyster shell to both soft bottom and vegetated habitats (Minello 1999; Stunz and Minello 2001; Stunz et al. 2002). In addition to the importance of physical structure there are a number of biotic (competition and predation) and abiotic (salinity and temperature) factors that can affect the assemblage structure of fish (Dunson and Travis 1991; Craig and Crowder 2000).

In Barataria Bay, changes in the physical/chemical properties of the water due to salt-water intrusion, a result of land loss, and by the introduction of freshwater, through such projects as the Davis Pond Diversion Project, which diverts Mississippi River waters directly into the bay's upper reaches, are also likely affecting the distribution and habitat use of fishes.

Physical/chemical properties of the water have been shown to be important factors affecting the spatial and temporal changes in fish species distribution, abundance and fish assemblage structure (Felly 1987; Peterson and Ross 1991; Rakocinski et al. 1992; Gelwick et al. 2001;

Jones et al; 2002). Specifically, salinity and temperature have been reported to be important predictors of freshwater and estuarine species presence and richness (Peterson and Ross 1991) and seasonal variations in species diversity and assemblage structure have been shown to be correlated with changes in depth, DO, salinity and temperature (Gelwick et al. 2001).

Since 1996, there has been an effort toward moving away from short-term single species management practices in coastal and marine systems towards an ecosystem approach of monitoring and managing these areas (Sherman and Duda 1999). This is due to the Sustainable Fisheries Act (SFA), an amendment of the Magnuson-Stevens Fishery Conservation and Management Act, which mandated the description and identification of essential fish habitat (EFH) for all fisheries under federal fisheries management. In the act, EFH is defined as ‘those waters and substrate necessary to fish for spawning, breeding, feeding or growth to maturity’ (NMFS 1997). Additionally, the SFA called for the National Marine Fisheries Service to assess the extent to which fisheries management and research are based upon ecosystem principles, and for a recommendation as to which ecosystem principles can be implemented further to improve marine resource management. Babcock and Pikitch (2004) point out that there is not yet a standardized approach to ecosystem based fisheries management, although some strategies that have been considered are: a suite of single species reference points, measures of ecosystem function (diversity), marine protected areas, gear restrictions and community based management. Therefore, a high level of data detailing the use and dependence of various habitat types and physical/chemical gradients is required to determine which habitats are supporting richer, more abundant and potentially more productive fish assemblages. Coen et al. (1999) point out the importance of simply differentiating between habitats that are utilized by transient and facultative resident finfish and crustaceans from habitats that should fall under EFH.

Thus by adopting the federal approach to fisheries management, the objective of this study was to investigate the fish assemblage structure in Barataria Bay, a portion of the Barataria-Terrebonne Basin experiencing the greatest amount of land loss in Louisiana, and to attempt to identify and describe EFH in this region. This study goes beyond a single species approach to identifying and describing EFH and investigates the habitat use of the Barataria Bay fish assemblage by investigating species composition, richness, relative abundance and biomass among marsh edge, soft bottom and oyster shell habitats, and in relation to the physical/chemical properties of the water.

## **Methods and Materials**

### Study Area

All collections were made in Barataria Bay, part of the Barataria-Terrebonne Estuarine Basin (BTEB) in coastal Louisiana (Figure 3.1). The BTEB encompasses an area of approximately 16,575 square kilometers within the Mississippi Deltaic Plain. The basin is bordered by the Mississippi River to the east, the East Atchafalaya Basin Levee and Atchafalaya River on the west and the Gulf of Mexico to the south. Three sites within Barataria Bay: Fisherman's Point (29°31'50"N 90°05'00"W), Manilla Village (29°25'74"N 89°59'20"W), and Grand Terre/Queen Bess (29°17'20"N 89°55'90"W/29°18'42"N 89°57'70"W respectively) were sampled to characterize fish assemblage richness, diversity, composition, distribution, relative abundance and biomass in Barataria Bay. The salinity ranges from oligohaline to mesohaline to polyhaline among Fisherman's Point, Manilla Village, and Grand Terre/Queen Bess, respectively. These sites were chosen because they represented a range in salinity, and each contained the three habitat types of interest: marsh edge, soft bottom (mud/sand) and oyster shell.

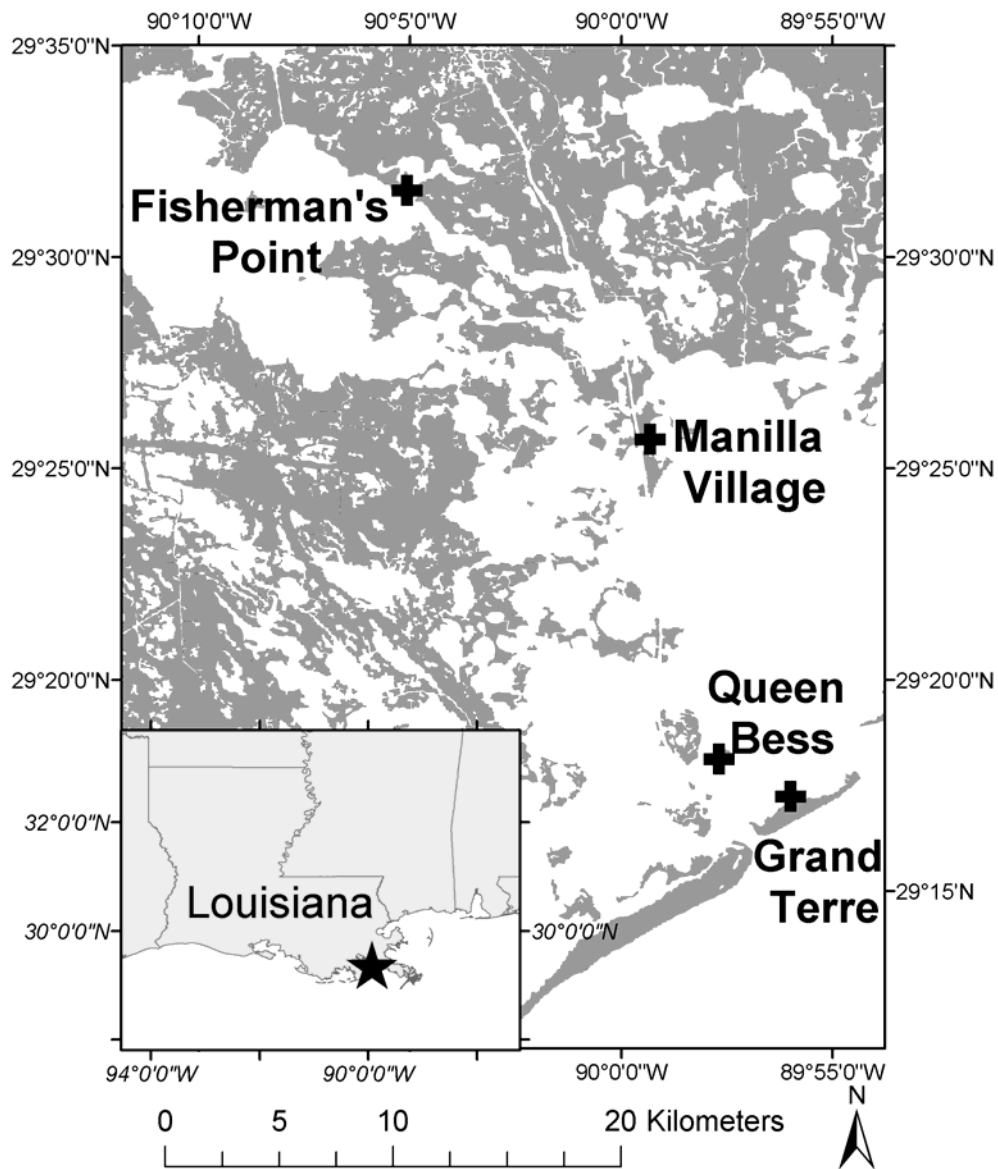


Figure 3.1. Map of Barataria Bay, Louisiana, and sampling sites: Grand Terre, Queen Bess, Manilla Village and Fisherman's Point.

Since the Grand Terre site did not have oyster shell habitat Queen Bess Island, a nearby location, was chosen to represent the oyster shell habitat for the polyhaline site. Although shell density differed at the three sites sampled, the within site variability was the comparison of interest. Klein digital side-scan sonar was used in an earlier study to differentiate oyster shell bottom from soft bottom (mud/sand). The swath format of the side-scan sonar provided a two dimensional acoustic image of bottom hardness (reflectance), surface texture (roughness) and topography. Habitat specific sampling locations were chosen based on these side-scan surveys (see Figures 1.2 to 1.5). In addition, SCUBA collections of bottom sediments was used to confirm bottom type of habitats.

### Sampling Protocol

Monthly sampling began in May 2003 and was completed in May 2004, with the exception of December 2003, which was not sampled due to inclement weather. Physical/chemical properties of the water were collected at each site on each sampling trip. Water temperature (°C), salinity (ppt) and dissolved oxygen (mg/L) data were collected with a YSI model 85 about 30 cm below the waters surface. Physical/chemical data were collected only at the site level given the close proximity of habitat types within each site. All fish were collected with a 46.5 m x 2.48 m gill net in the soft bottom and oyster shell habitat, and a 46.5 m x 1.24 m gill net in the marsh edge habitat due to the shallower depth of the water at the marsh perimeter. All nets consisted of five 9.3 m panels, with the following bar mesh sizes: 1.27, 1.91, 2.54, 3.18 and 3.81 cm. One gill net was set per habitat type per site for one hour. Fish were collected after one hour, and then the nets were reset in the same place for another hour to replicate the sample in time. Fish were put in an ice slurry with MS 222, and then bagged and left on ice to be frozen

later. In the laboratory all fish were weighed to the nearest 0.1 gram, measured for standard length to the nearest 0.1 centimeter and recorded by site and habitat.

### Statistical Analyses

An analysis of variance (ANOVA) (SAS Institute 2002) was used to test whether the physical/chemical properties of the water differed among sites and months. Variables that were significant at the level of  $\alpha=0.05$  were further tested with a Tukey HSD post-ANOVA test to determine which variables contributed to observed differences. Note that month was nested within year for this analysis because of the overlap between May 2003 and May 2004.

Species richness was calculated from the number of species present at a given site and/or habitat per month, and therefore was a combination of the two replicates. An ANOVA (SAS Institute 2002) was used to test whether species richness differed among habitats and sites, or in relation to any of the physical/chemical properties of the water. In this analysis the variable month(year) was replaced by the co-variables temperature, salinity and dissolved oxygen, since these factors differed significantly among months. As in chapter one the interactions (temperature by site, salinity by site and dissolved oxygen by site) were excluded to keep the model consistent throughout the dissertation. Thus the simplified model of site, habitat, temperature, salinity, dissolved oxygen and site by habitat was then used for all tests of significance in this chapter. Variables that were significant at the level of  $\alpha=0.05$  were further tested with a Tukey HSD post-ANOVA test to determine which variables contributed to observed differences.

An ANOVA (SAS Institute 2002) was used to test whether catch per unit effort (CPUE) and biomass of all species combined differed among sites and habitats, or in relation to physical/chemical properties of the water. Variables that were significant at the level of  $\alpha=0.05$ , were further tested with a Tukey HSD post-ANOVA test to determine which

variables contributed to the observed difference. Rare species, those species collected three or fewer times, were removed from the analysis as they contributed little to the overall tests. Additionally, an ANOVA on CPUE was run excluding Gulf menhaden, *Brevoortia patronus*, given the predominance of this species in the catch. This was not the case in total biomass and therefore an additional analysis was not performed for this portion. A multiple analysis of variance (MANOVA) (SAS Institute 2002) was used to test whether CPUE and biomass of individual species differed among habitats and sites, or in relation to physical/chemical properties of the water. Variables that were significant at the level of  $\alpha=0.05$ , were further tested with a Tukey HSD post-ANOVA test to determine which variables contributed to the observed difference. CPUE and biomass data were  $\log(x + 1)$  transformed prior to analysis because the raw data were not normally distributed. Due to time constraints and selection criteria of sampling sites, treatments were not replicated and therefore caution should be used when extrapolating results to areas other than those sampled during this project (Hurlbert 1984).

Correspondence analysis (CA) was used to summarize different types of underlying structure of the fish assemblage and to determine if patterns in fish assemblage structure differed among sites and habitats. A CA is a graphical representation of the associations in a table of frequency or counts, which plots these associations in low dimensional space (Johnson and Wichern 2002). Points in the plot that are close together represent points of similar profiles, e.g., sites close together represent sites with similar fish assemblage structure. CA was performed with presence/absence data from May to October 2003 to highlight species composition when most species were present in Barataria Bay. The CA's did not include rare species, as they have been shown to offer little information about the underlying data structure in ordination analyses (Gauch 1982). Thus only those species collected more than three times during the study were

included. In addition, the skipjack herring, *Alosa chrysochloris*, was excluded from the CA's because it was an outlier and contributed little to the explanative value of the analysis (Gauch 1982).

Canonical correspondence analysis (CCA) was used to relate fish assemblage structure to habitat type and physical/chemical properties of the water. Data include all sampling dates from May 2003 to May 2004. Rare species (those collected three and fewer times over that period) and the outliers skipjack herring and black drum were removed from this analysis because they contributed little to the explanative value of the analysis. A CCA is an example of a multivariate direct gradient analysis (Ter Braak 1986). A CCA relates environmental variables to fish assemblage structure by imposing a restriction that the species ordination axes be linear combinations of environmental variables (Ter Braak 1986). This analysis results in an ordination plot where points representing species and vectors representing environmental variables are overlaid. The distance between species approximates the dissimilarity of distribution of relative abundance of those species across samples, measured by their chi-square distance (Ter Braak and Smilauer 2002). As such, species found close to one another commonly co-occur. Environmental variable vectors point in the expected direction of the steepest increase in value of environmental variables, while the angles between vectors represent correlation between the environmental variables (Ter Braak and Smilauer 2002). The perpendicular distance of the species points from the environmental vectors can then be used to approximate the optima for each species in respect to each environmental variable (Ter Braak and Smilauer 2002). A Monte Carlo test was then employed on the first canonical axis and then for all four canonical axes, as a test of significance between the species-environmental relationships.

## **Results**

### Physical/Chemical Data

Water temperature was highest between May and October, but ranged between 10.4°C and 32.1°C throughout the year (Figure 3.2). Temperature was generally inversely related to dissolved oxygen, which was highest between January and April, and ranged between 5.0 mg/L to 10.9 mg/L throughout the year (Figure 3.3). Temperature and dissolved oxygen did not differ significantly between sites ( $p = 0.06$ ,  $p = 0.68$  respectively; Table 3.1), but did differ significantly between months sampled ( $p < 0.05$ ,  $p < 0.05$ , respectively; Table 3.1). Salinity fluctuated throughout the year and ranged between 0.7 ppt to 29.6 ppt (Figure 3.4). Salinity differed significantly between sites ( $p < 0.05$ ; Table 3.1) and months sampled ( $p < 0.05$ ; Table 3.1). A Tukey HSD post-ANOVA test indicated that salinity at the Grand Terre and Queen Bess sites were not significantly different from one another, which validated the inclusion of Queen Bess as a substitute shell habitat for the Grand Terre site. In addition, the Tukey HSD post-ANOVA test significantly separated the polyhaline sites Grand Terre and Queen Bess from the mesohaline site Manilla Village, and the oligohaline site Fisherman's Point.

### Species Richness

Thirty-eight species in 18 families were collected in Barataria Bay between May 2003 and May 2004 (Table 3.2, Appendix 1, 2 and 3). Species richness varied significantly amongst sites and habitats and in relation to physical/chemical properties of the water (Table 3.3). Species richness was significantly higher at Grand Terre/Queen Bess and Manilla Village as compared to Fisherman's Point ( $p < 0.001$ , Table 3.4) and was significantly higher at the oyster shell habitat than the marsh edge habitat ( $p = 0.03$ , Table 3.4). The soft bottom habitat was not significantly different than either the oyster shell or marsh edge habitats (Table 3.4). There was a significant

site by habitat interaction ( $p = 0.03$ , Tables 3.3 and 3.5, Figures 3.5, 3.6 and 3.7), which indicates that the main effects may not be independent. Species richness was also significantly related to water temperature and salinity ( $p < 0.001$ ,  $p = 0.01$ , respectively, Table 3.2), where richness increased as both water temperature (Figure 3.8) and salinity (Figure 3.10) increased. Species richness was not significantly related to dissolved oxygen, but generally decreased as dissolved oxygen increased (Figure 3.9).

Table 3.1. Results from analysis of variance comparing water temperature, dissolved oxygen and salinity by site and month(year).

	d.f.	F	MS	p-value
<b>Temperature</b>				
Site	3	2.69	2.26	0.06
Month(year)	11	177.48	149.17	<0.05
<b>Salinity</b>				
Site	3	111.68	518.92	<0.05
Month(year)	11	16.38	76.09	<0.05
<b>Dissolved oxygen</b>				
Site	3	0.50	0.36	0.68
Month(year)	11	11.95	8.52	<0.05

Table 3.2. List of collected species by common and scientific name, family and species codes used in correspondence and canonical correspondence analyses.

Common	Scientific	Family	Species code
Alligator gar	<i>Lepisosteus spatula</i>	Lepisosteidae	AG
Atlantic croaker	<i>Micropogonias undulatus</i>	Sciaenidae	AC
Atlantic cutlassfish	<i>Trichiurus lepturus</i>	Trichiuridae	ACF
Atlantic needlefish	<i>Strongylura marina</i>	Belonidae	AN
Atlantic threadfin herring	<i>Opisthonema oglinum</i>	Clupeidae	ATH
Bay whiff	<i>Citharichthys spilopterus</i>	Bothidae	BW
Bighead searobin	<i>Prionotus tribulus</i>	Triglidae	BHS
Black drum	<i>Pogonias cromis</i>	Sciaenidae	BD
Bull shark	<i>Carcharhinus leucas</i>	Carcharhinidae	BS
Cobia	<i>Rachycentron canadum</i>	Rachyentridae	CB
Crevalle jack	<i>Caranx hippos</i>	Carangidae	CJ
Florida pompano	<i>Trachinotus carolinus</i>	Carangidae	FP
Gafftopsail catfish	<i>Bagre marinus</i>	Ariidae	GC
Gizzard shad	<i>Dorosoma cepedianum</i>	Clupeidae	GS
Gulf menhaden	<i>Brevoortia patronus</i>	Clupeidae	GM
Inshore lizardfish	<i>Synodus foetens</i>	Sydontidae	IL
Ladyfish	<i>Elops saurus</i>	Elopidae	LF
Leather jacket	<i>Oligoplites saurus</i>	Carangidae	LJ
Pinfish	<i>Lagodon rhomboides</i>	Sparidae	PF
Red drum	<i>Sciaenops ocellatus</i>	Sciaenidae	RD

Table 3.2 Cont'd.

Common	Scientific	Family	Species code
Sand seatrout	<i>Cynoscion arenarius</i>	Sciaenidae	SDS
Scaled sardine	<i>Harengula jaguana</i>	Clupeidae	SCS
Sea catfish	<i>Arius felis</i>	Ariidae	HC
Sheepshead	<i>Archosargus probatocephalus</i>	Sparidae	SH
Silver perch	<i>Bairdiella chrysoura</i>	Sciaenidae	SLP
Skipjack herring	<i>Alosa chrysochloris</i>	Clupeidae	SJ
Southern flounder	<i>Paralichthys lethostigma</i>	Bothidae	SF
Southern kingfish	<i>Menticirrhus americanus</i>	Sciaenidae	SK
Spanish mackerel	<i>Scomberomorus maculatus</i>	Scombridae	SPM
Spot	<i>Leiostomus xanthurus</i>	Sciaenidae	SP
Spotfin mojarra	<i>Eucinostomus argenteus</i>	Gerreidae	SF
Spotted gar	<i>Lepisosteus oculatus</i>	Lepisosteidae	SG
Spotted seatrout	<i>Cynoscion nebulosus</i>	Sciaenidae	SPS
Striped anchovy	<i>Anchoa hepsetus</i>	Engraulidae	STA
Striped mullet	<i>Mugil cephalus</i>	Mugilidae	SM
Threadfin shad	<i>Dorosoma petenense</i>	Clupeidae	TS
White mullet	<i>Mugil curema</i>	Mugilidae	WM

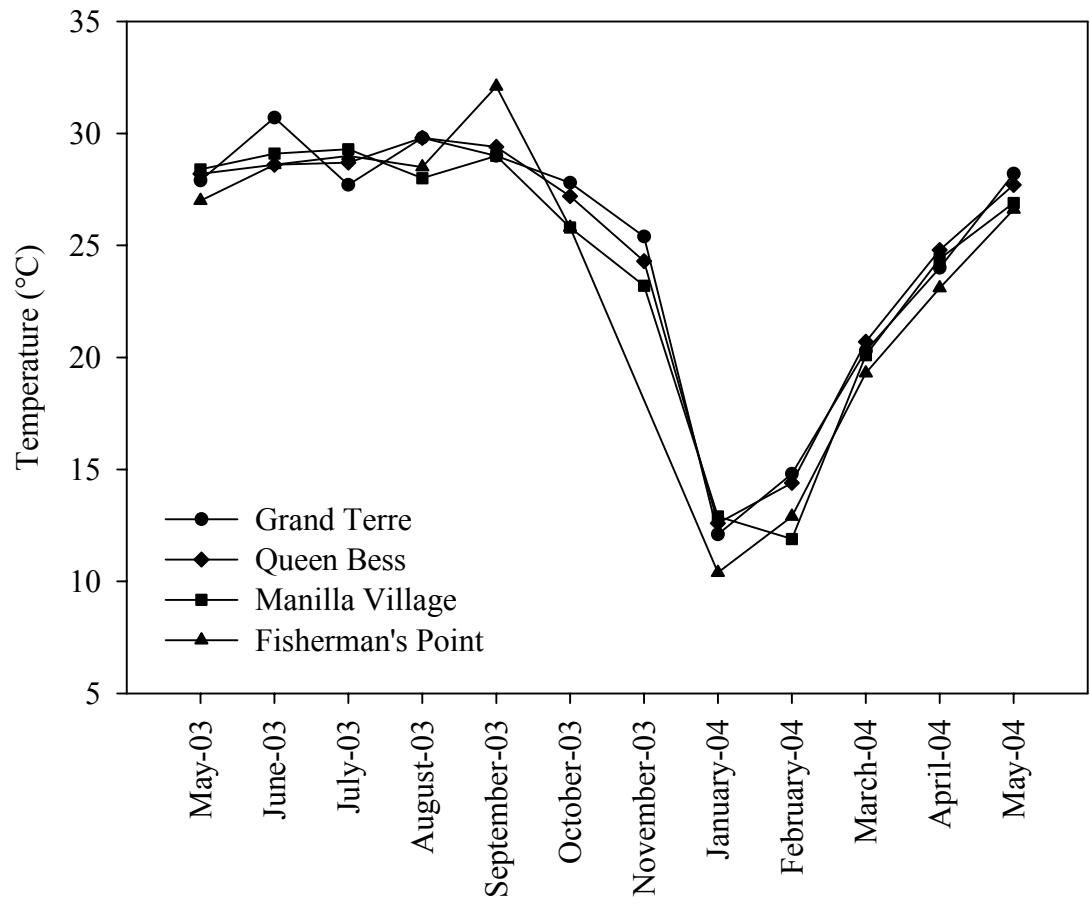


Figure 3.2. Water temperature (°C) by site for May 2002 to May 2004.

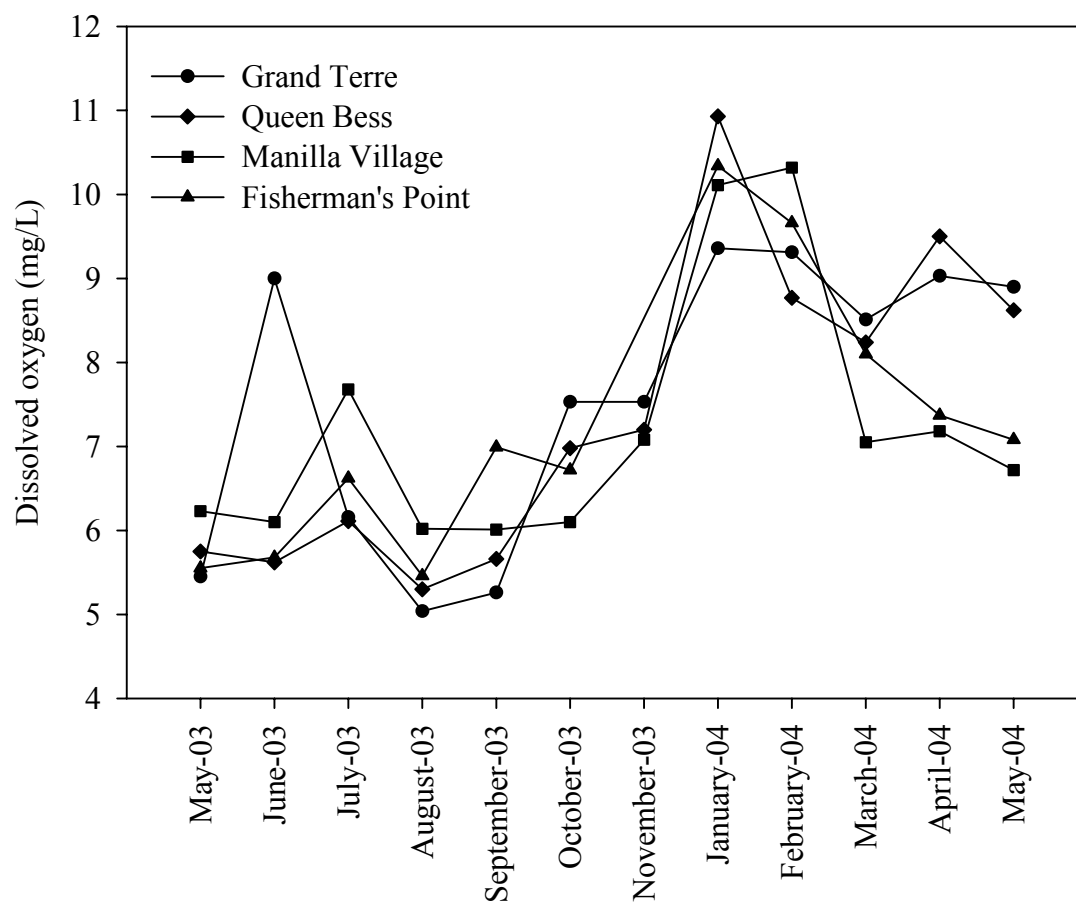


Figure 3.3. Dissolved oxygen (mg/L) by site for May 2002 to May 2004.

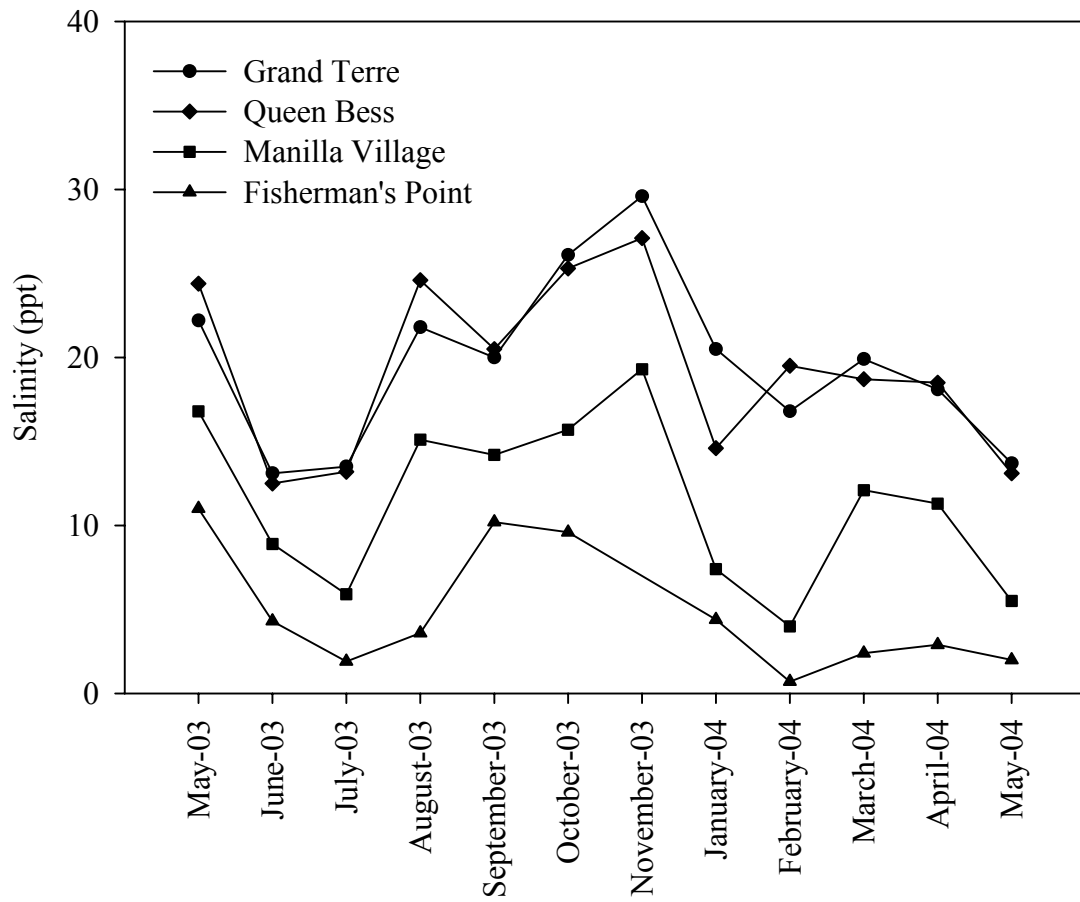


Figure 3.4. Salinity (ppt) by site for May 2002 to May 2004.

Table 3.3. Analysis of variance of fish species richness, the number of fish species collected, among the three sites and habitats sampled.

Species richness	MS	F	d.f.	p-value
Site	67.42	11.00	2	< 0.001
Habitat	21.63	3.53	2	0.03
Temperature	78.81	12.86	1	< 0.001
Salinity	38.98	6.36	1	0.01
Dissolved oxygen	18.69	3.05	1	0.08
Site x habitat	17.84	2.91	4	0.03

Table 3.4. Tukey HSD post-ANOVA test on fish species richness, the number of fish species collected, among the three sites and habitats sampled. Different letters indicate a significant difference.

Tukey HSD	Richness	N	Site
A	6.5	35	Grand Terre/Queen Bess
A	6.4	36	Manilla Village
B	4.1	33	Fisherman's Point
B	5.0	34	Marsh edge
AB	5.4	35	Soft bottom
A	6.5	35	Oyster shell

Table 3.5. Results from Tukey HSD post-2 way ANOVA test of effects comparing richness by site and habitat. Different letters indicate a significant difference.

Richness	Marsh edge	Soft bottom	Oyster shell
Grand Terre/Queen Bess	7.99±0.90 AB	7.70±0.88 AB	6.83±0.85 AB
Manilla Village	5.09±0.72 ABC	5.59±0.71 ABC	6.83±0.85 AB
Fisherman's Point	1.70±0.87 C	2.98±0.87 BC	4.43±0.87 ABC

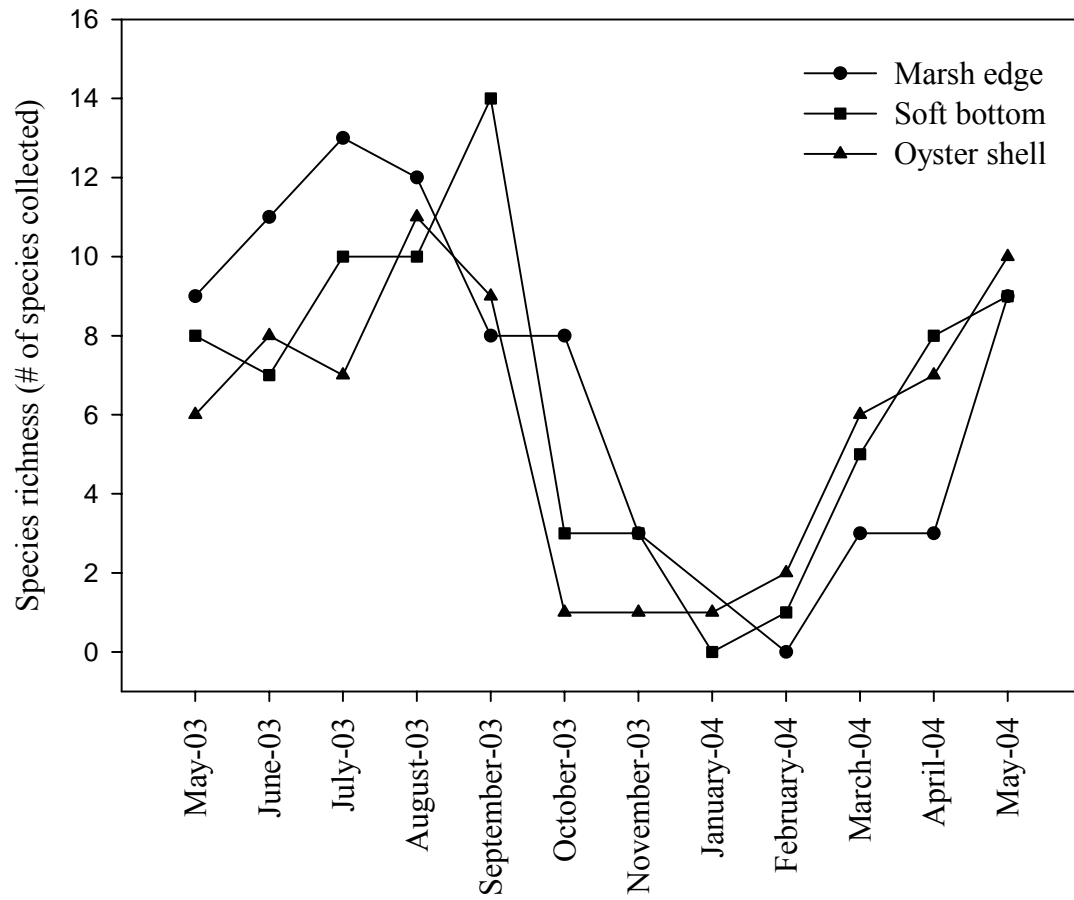


Figure 3.5. Species richness at Grand Terre/Queen Bess by habitat type from May 2003 to May 2004.

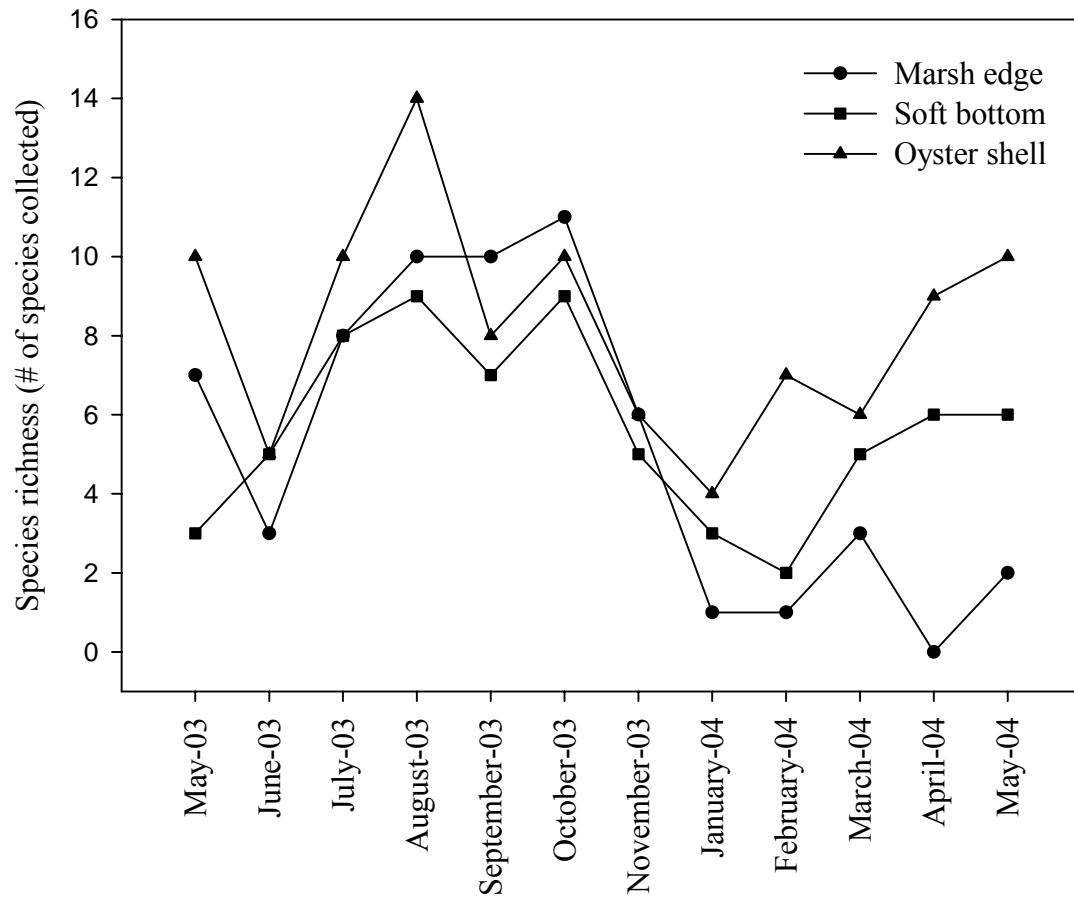


Figure 3.6. Species richness at Manilla Village by habitat type from May 2003 to May 2004.

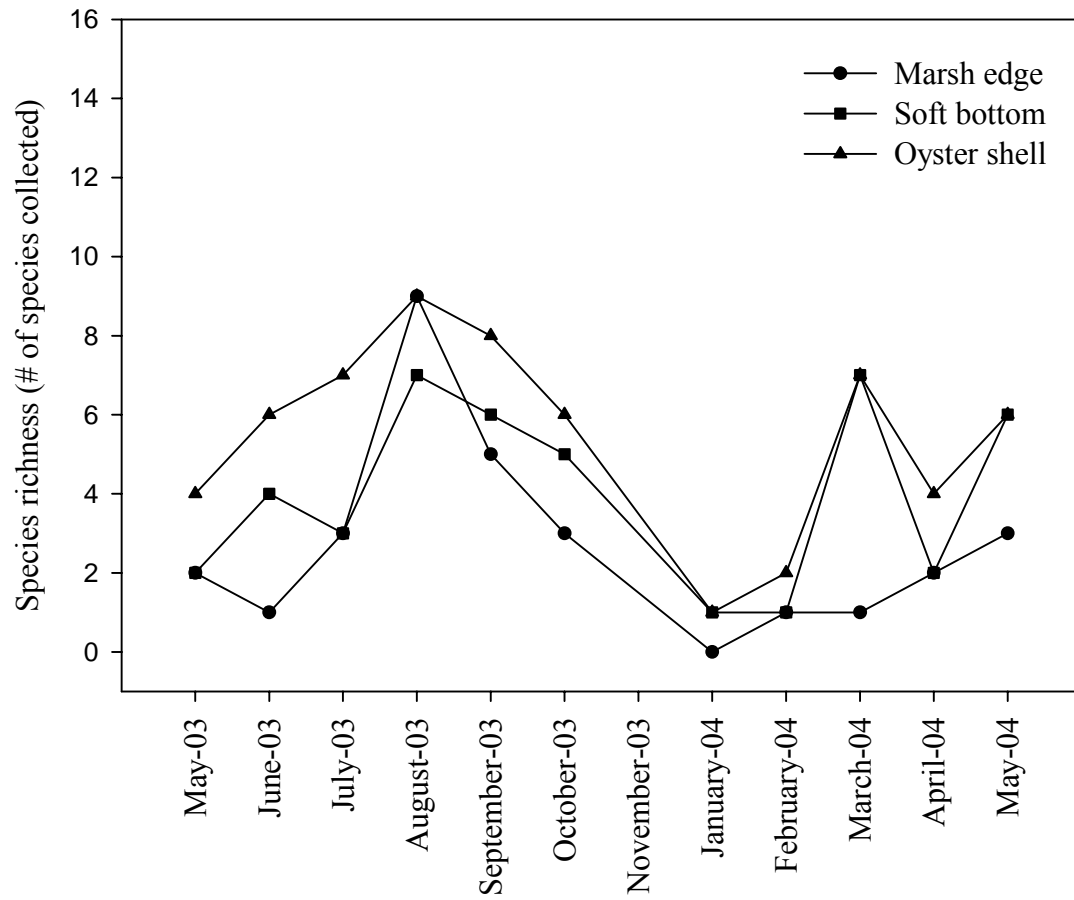


Figure 3.7. Species richness at Fisherman's Point by habitat type from May 2003 to May 2004.

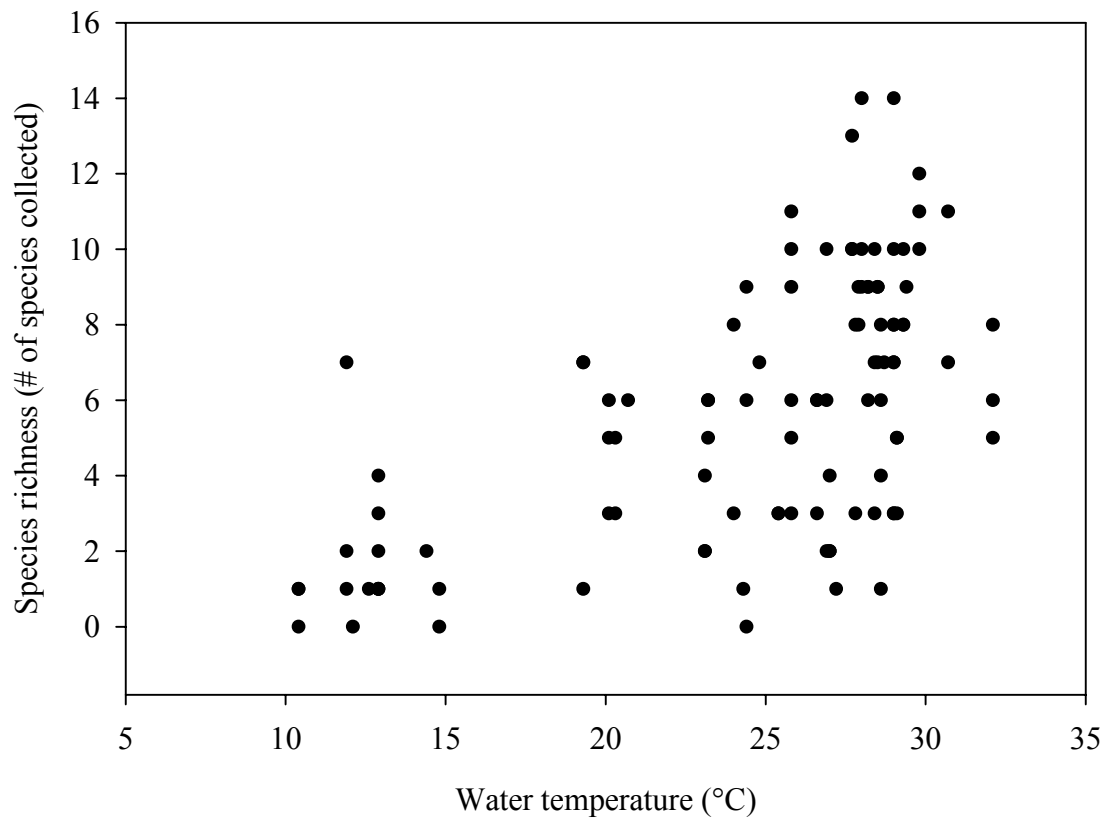


Figure 3.8. Relationship between species richness and water temperature (°C) for all sites combined from May 2003 to May 2004.

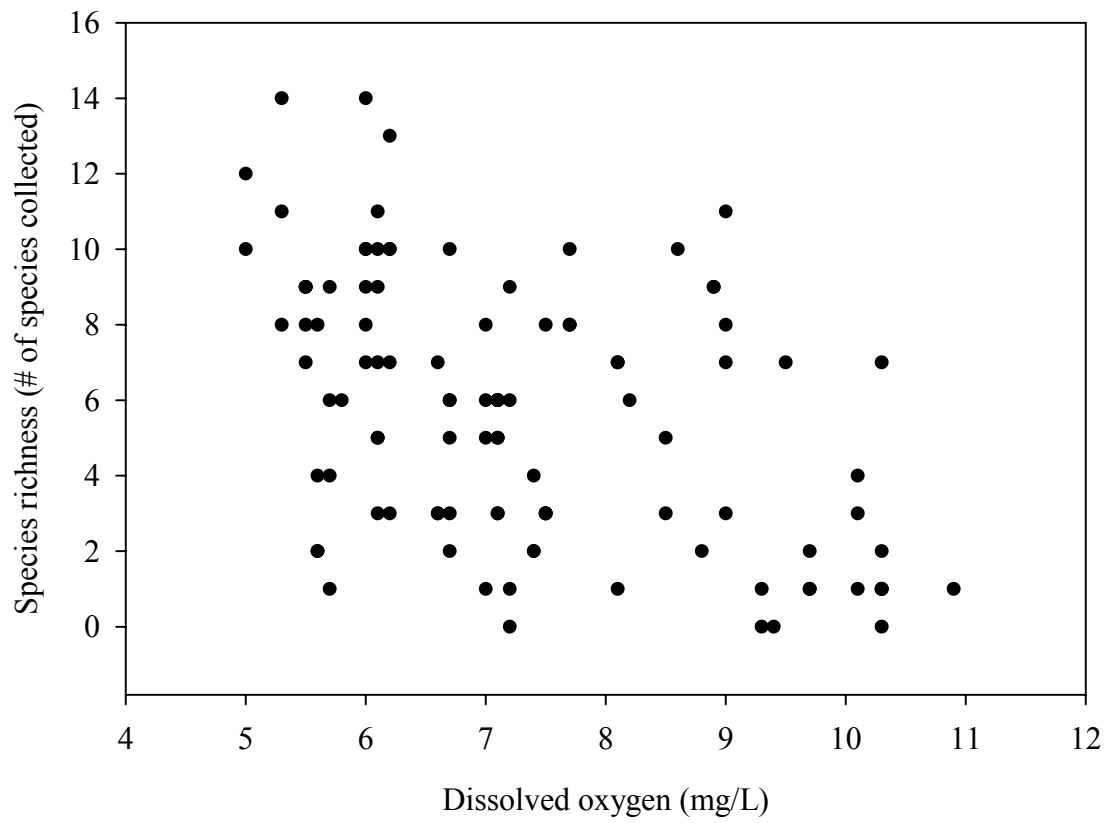


Figure 3.9. Relationship between species richness and dissolved oxygen (mg/L) for all sites combined from May 2003 to May 2004.

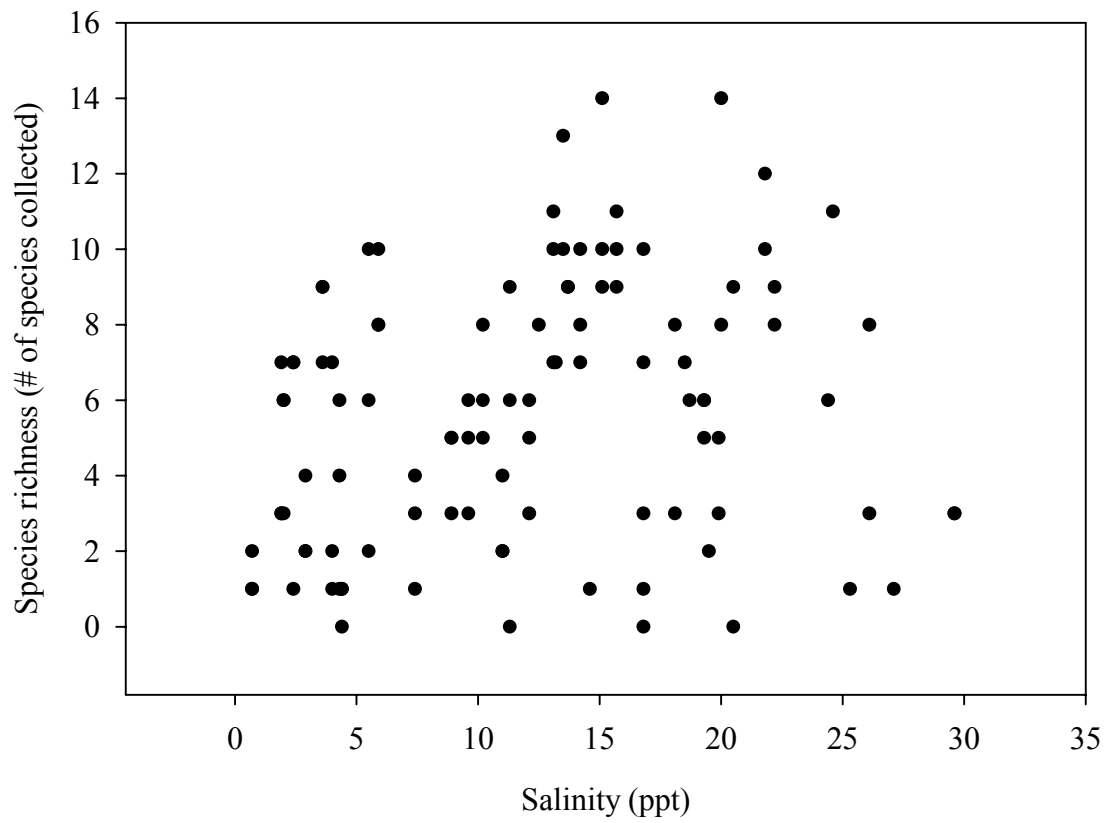


Figure 3.10. Relationship between species richness and salinity (ppt) for all sites combined from May 2003 to May 2004.

## Relative Abundance

A total of 7,098 fish were collected in Barataria Bay between May 2003 and May 2004. The most abundant species collected was the Gulf menhaden, representing 61.2% of the total catch. The next most abundant species was the spot, *Leiostomus xanthurus*, at 6.8%, followed by Atlantic croaker, *Micropogonias undulatus*, at 4.3%, silver perch, *Bairdiella chrysoura*, at 4.2% and scaled sardine, *Harengula jaguana*, at 4.1%. All other species each contributed less than 4.0% of total catch. CPUE of all species combined varied significantly among sites and habitats, and in relation to physical/chemical properties of the water (Table 3.6). The Tukey HSD post-ANOVA test indicated that CPUE of all species combined was significantly higher at Grand Terre/Queen Bess and Manilla Village than Fisherman's Point, and was significantly higher at the oyster shell and soft bottom habitats than at the marsh edge habitat (Table 3.7). There was a significant site by habitat interaction ( $p < 0.001$ , Tables 3.6 and 3.8, Figures 3.11, 3.12 and 3.13), which indicates that the main effects may not be independent. CPUE was also significantly related to water temperature, salinity and dissolved oxygen (Table 3.6), where CPUE generally increased as temperature and salinity increased (Figures 3.14 and 3.16), and generally decreased as dissolved oxygen increased (Figure 3.15). Because Gulf menhaden made up over 61% of the total catch, they were removed from the data set to determine if trends in catch among sites, habitats and physical/chemical properties differed if Gulf menhaden were included. Results indicate that the removal of Gulf menhaden did not change the overall interpretation of results ( $p < 0.02$ , Table 3.9).

Table 3.6. Analysis of variance of log (CPUE + 1) of all fish species combined, among the three sites and habitats sampled. CPUE based upon one hour gill net set.

Log (CPUE + 1)	d.f.	F	MS	p-value
Site	2	15.99	18.80	< 0.001
Habitat	2	24.32	28.60	< 0.001
Temperature	1	8.09	9.51	< 0.005
Salinity	1	14.39	16.92	< 0.001
Dissolved oxygen	1	15.42	18.13	< 0.001
Site x habitat	4	10.98	12.91	< 0.001

Table 3.7. Tukey HSD post-ANOVA test of log (CPUE + 1) of all fish species combined, among the three sites and habitats sampled. CPUE based on one hour gill net set. Different letters indicate a significant difference.

Tukey HSD	Log (CPUE + 1)	N	Site
A	2.6	70	Grand Terre/Queen Bess
A	2.7	71	Manilla Village
B	1.9	66	Fisherman's Point
B	1.7	68	Marsh edge
A	2.8	69	Soft bottom
A	2.8	70	Oyster shell

Table 3.8. Tukey HSD post-2 way ANOVA test of effects of log (CPUE + 1) of all fish species combined comparing by site and habitat. Different letters indicate a significant difference.

log (CPUE + 1)	Marsh edge	Soft bottom	Oyster shell
Grand Terre/Queen Bess	3.25±0.28 ABC	3.59±0.27 AB	2.74±0.26 ABC
Manilla Village	1.41±0.22 DE	2.76±0.23 ABC	3.69±0.22 A
Fisherman's Point	0.36±0.27 E	1.94±0.27 CD	2.02±0.27 BCD

Table 3.9. Analysis of variance of log (CPUE + 1) of all fish species combined excluding Gulf menhaden, among the three sites and habitats sampled. CPUE based on one hour gill net set.

log (CPUE + 1)	d.f.	F	MS	p-value
Site	2	19.23	16.23	< 0.001
Habitat	2	5.84	4.92	0.004
Temperature	1	13.09	11.05	< 0.001
Salinity	1	6.13	5.17	0.01
Dissolved oxygen	1	5.59	4.71	0.02
Site x habitat	4	8.69	7.33	< 0.001

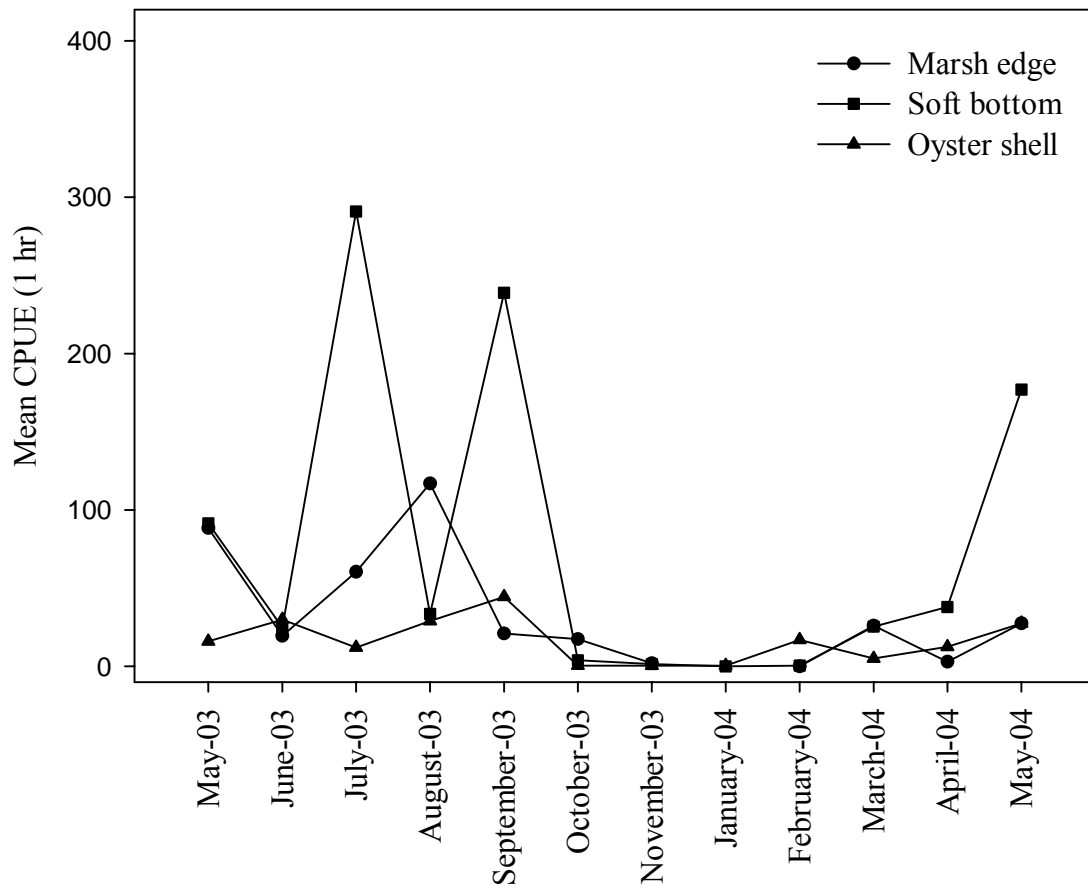


Figure 3.11. Mean catch per unit effort by habitat type, per one hour gill net soak, at Grand Terre/ Queen Bess from May 2003 to May 2004.

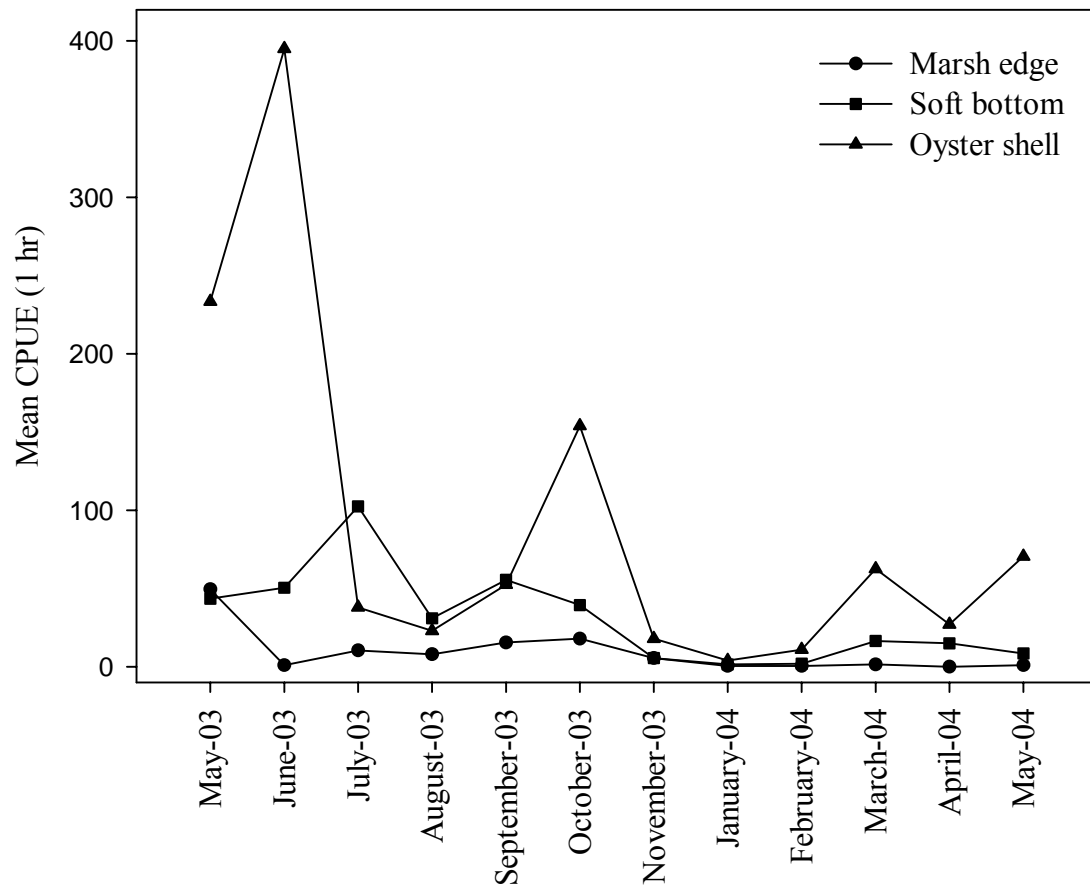


Figure 3.12. Mean catch per unit effort by habitat type, per one hour gill net soak, at Manilla Village from May 2003 to May 2004.

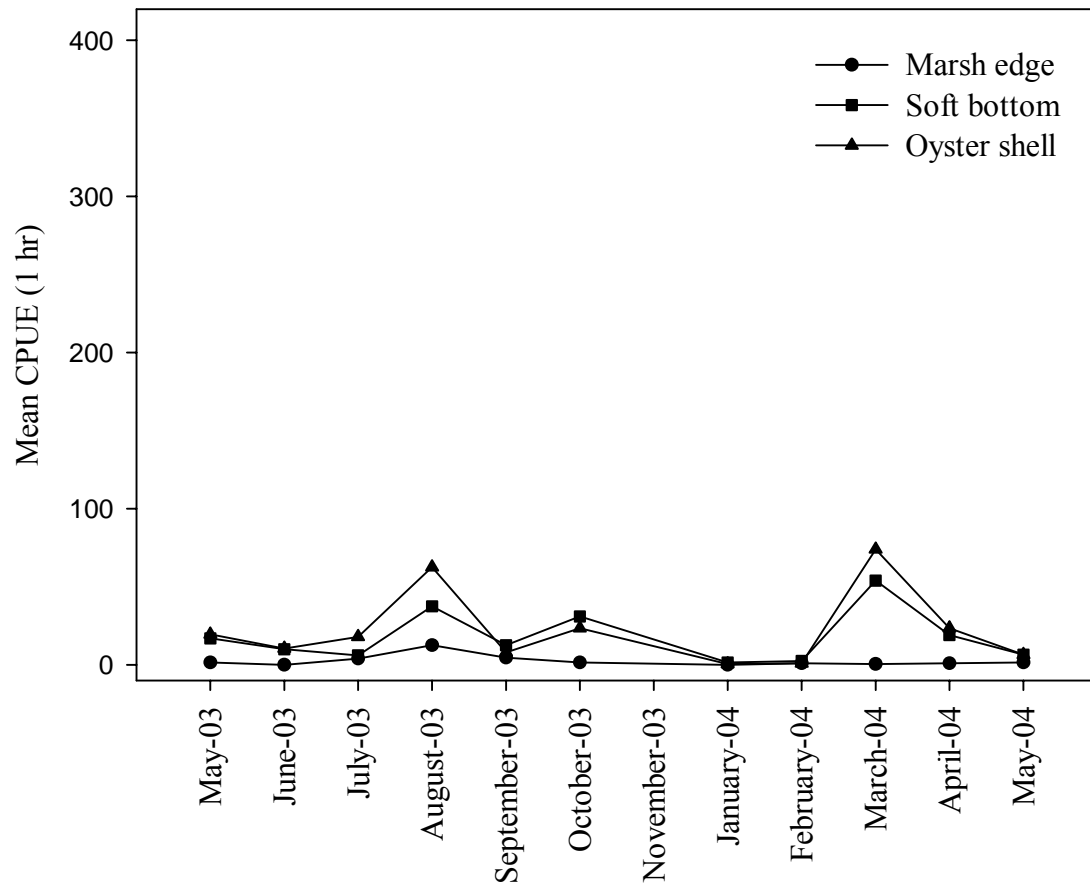


Figure 3.13. Mean catch per unit effort by habitat type, per one hour gill net soak, at Fisherman's Point from May 2003 to May 2004.

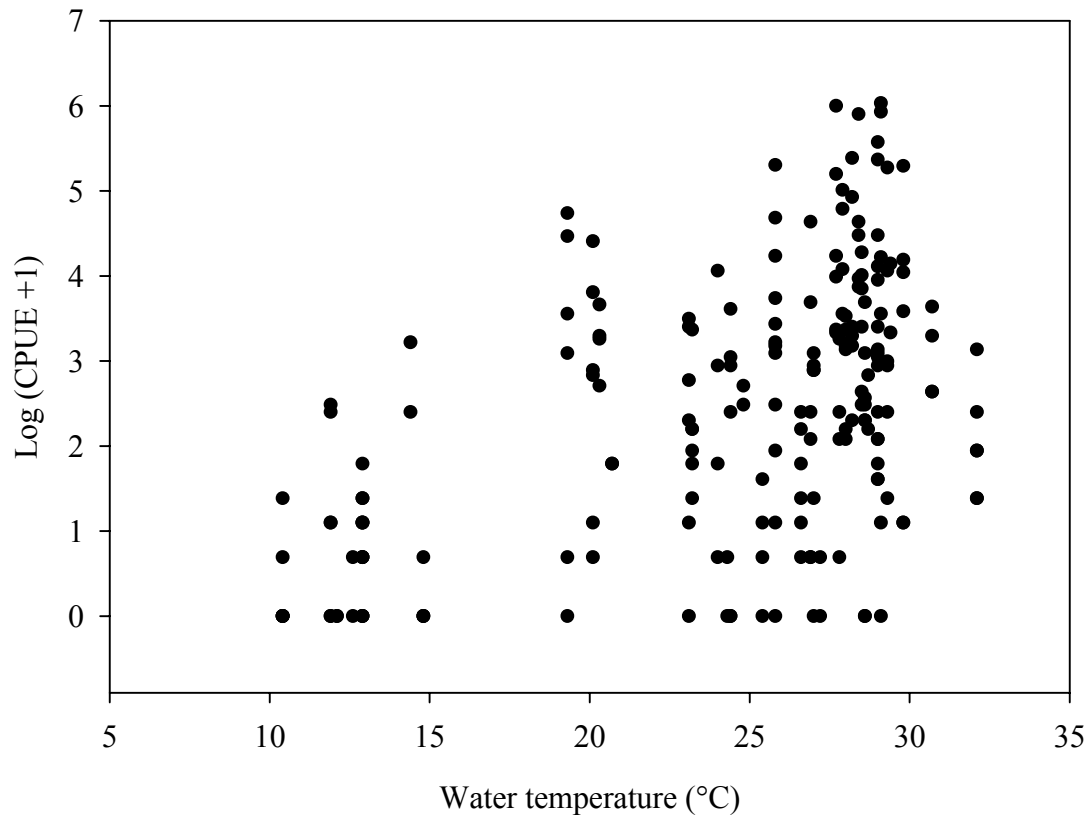


Figure 3.14. Relationship between catch per unit effort and water temperature (°C) for all sites combined from May 2003 to May 2004.

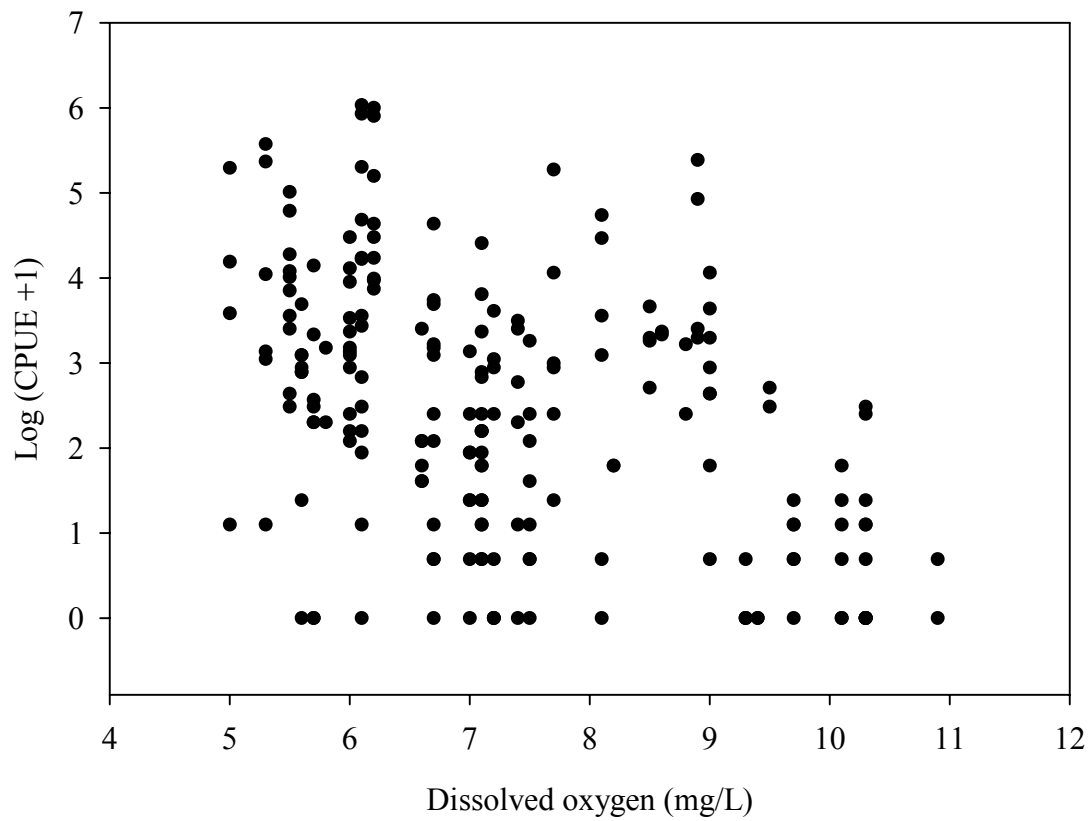


Figure 3.15. Relationship between catch per unit effort and dissolved oxygen (mg/L) for all sites combined from May 2003 to May 2004.

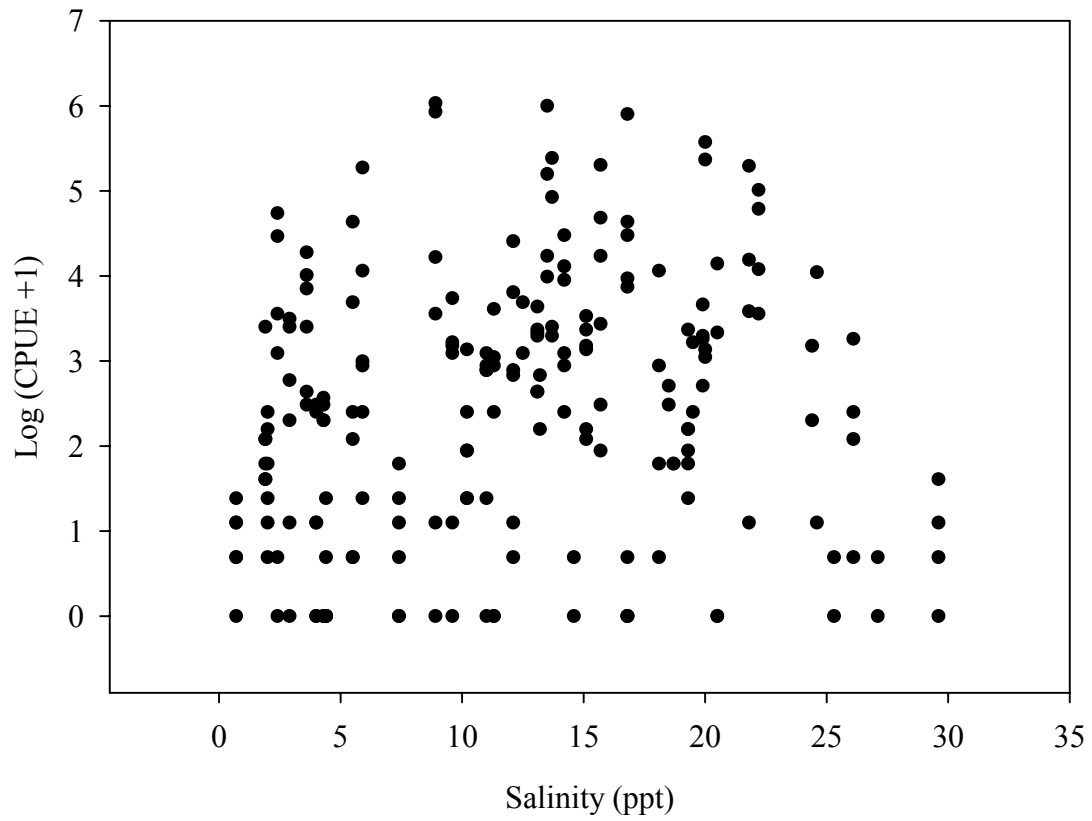


Figure 3.16. Relationship between catch per unit effort and salinity (ppt) for all sites combined from May 2003 to May 2004.

### Species-Specific Relative Abundance

The MANOVA results supported the ANOVA of log (CPUE + 1) indicating a significant relationship between CPUE and site, habitat, temperature, salinity, dissolved oxygen and site by habitat interaction (Table 3.10). The benefit of this analysis over the ANOVA is that it allows for the examination of which species contributed to observed differences. The Tukey HSD post-ANOVA test among sites indicated that the CPUE of 11 of the 25 most common species did not differ among sites (Table 3.11). The Atlantic croaker, spot, crevalle jack, *Caranx hippos*, southern kingfish, *Menticirrhus americanus*, and the pinfish, *Lagodon rhomboides*, had a higher CPUE at Grand Terre/Queen Bess site than the other two sites, while the sand seatrout, *Cynoscion arenarius*, and spotted seatrout, *Cynoscion nebulosus*, had a higher CPUE at both Grand Terre/Queen Bess and Manilla Village than Fisherman's Point. The Spanish mackerel, *Scomberomorus maculatus*, was the only species that had a CPUE that differed significantly among all sites, with CPUE decreasing from the polyhaline to the oligohaline site. The Atlantic needlefish, *Strongylura marina*, is the only species that was more abundant at Fisherman's Point than the other two sites sampled. The remaining species generally fell into two categories, those with a higher CPUE at Grand Terre/Queen Bess and Manilla Village as compared to Fisherman's Point (silver perch, Atlantic threadfin herring, *Opisthonema oglinum*, leather jacket, *Oligoplites saurus*, and scaled sardine) and those with a generally higher CPUE at Manilla Village and Fisherman's Point as compared to Grand Terre/Queen Bess (Gulf menhaden and gafftopsail catfish, *Bagre marinus*).

The Tukey HSD post-MANOVA test among habitats indicated that the CPUE of 18 of the 25 species did not differ among habitats (Table 3.12). The red drum, *Sciaenops ocellatus*, and striped mullet, *Mugil cephalus*, had a higher CPUE along the marsh edge as compared to the soft

bottom and oyster shell habitats, and the Gulf menhaden, sand seatrout and Spanish mackerel had higher CPUE at the soft bottom and oyster shell habitats as compared to the marsh edge habitat. Thus, in general species broke into three main groups, those not differing in abundance among habitats, those more abundant along the marsh edge and those most abundant in the open water habitat. However, the CPUE of silver perch was greater at the oyster shell habitat than the soft bottom habitat, although the CPUE at the marsh edge did not differ from either habitat. In addition, the southern kingfish had a higher CPUE at the soft bottom habitat than the marsh edge habitat, with the CPUE of southern kingfish at the oyster shell habitat not differing significantly from either the marsh edge or soft bottom habitats (Table 3.12).

Table 3.10. Multiple analysis of variance of log (CPUE + 1) for all fish collected, among the three sites and habitats sampled. CPUE is based upon one hour gill net set.

Log (CPUE+1)	d.f.	F	Wilks' Lambda	p-value
Site	50	3.61	0.43	< 0.001
Habitat	50	3.34	0.45	< 0.001
Temperature	25	3.99	0.063	< 0.001
Salinity	25	3.63	0.65	< 0.001
Dissolved oxygen	25	3.38	0.67	< 0.001
Site x habitat	100	1.71	0.41	< 0.001

Table 3.11. Tukey HSD post-MANOVA test of log (CPUE + 1) for all fish collected, among the three sites sampled. CPUE is based on a one-hour gill net set. Different letters along each row indicate a significant difference among sites for a given species.

Species	Grand Terre/ Queen Bess	Manilla Village	Fisherman's Point
Gizzard shad	A	A	A
Threadfin shad	A	A	A
Skipjack herring	A	A	A
Atlantic Croaker	A	B	B
Spot	A	B	B
Gulf Menhaden	B	A	AB
Sand seatrout	A	A	B
Sea catfish	A	A	A
Gafftopsail catfish	B	A	AB
Striped mullet	A	A	A
Silver perch	A	AB	B
Bighead searobin	A	A	A
Crevalle jack	A	A	A
Southern kingfish	A	B	B
Spotted seatrout	A	A	B
Ladyfish	A	A	A
Atlantic threadfin herring	A	AB	B
Black Drum	A	A	A

Table 3.11 Cont'd.

Species	Grand Terre/ Queen Bess	Manilla Village	Fisherman's Point
Red drum	A	A	A
Pinfish	A	B	B
Spanish mackerel	A	B	C
Scaled sardine	A	AB	B
Atlantic needlefish	B	B	A
Leather jacket	AB	A	B
White mullet	A	A	A

Table 3.12. Tukey HSD post-MANOVA test of log (CPUE + 1) for all fish collected among the three habitats. CPUE is based upon one hour gill net set. Different letters along each row indicate a significant difference among sites for a given species.

Species	Marsh edge	Soft bottom	Oyster shell
Gizzard shad	A	A	A
Threadfin shad	A	A	A
Skipjack herring	A	A	A
Atlantic Croaker	A	A	A
Spot	A	A	A
Gulf Menhaden	B	A	A
Sand seatrout	B	A	A
Sea catfish	A	A	A
Gafftopsail catfish	A	A	A
Striped mullet	A	B	B

Table 3.12 Cont'd.

Silver perch	AB	B	A
Bighead searobin	A	A	A
Crevalle jack	A	A	A
Southern kingfish	B	A	AB
Spotted seatrout	A	A	A
Ladyfish	A	A	A
Atlantic threadfin herring	A	A	A
Black Drum	A	A	A
Red drum	A	B	B
Pinfish	A	A	A
Spanish mackerel	B	A	A
Scaled sardine	A	A	A
Atlantic needlefish	A	A	A
Leather jacket	A	A	A
White mullet	A	A	A

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### Biomass

A total biomass of 353.5 kg of fish was collected between May 2003 and May 2004 in Barataria Bay. The biomass of Gulf menhaden predominated the catch and represented 27.9% of the total biomass. The sea catfish, *Arius felis*, represented 18.5% of the total biomass, followed by spotted seatrout at 11.5%, black drum at 7.0%, Spanish mackerel at 5.8% and the ladyfish, *Elops saurus*, at 4.6%. All other species each contributed no more than 4.0% to the total biomass. Total biomass varied significantly among sites and habitats and in relation to

physical/chemical properties of the water (Table 3.13). The Tukey HSD post-ANOVA test indicated that biomass of all species combined was significantly higher at Grand Terre/Queen Bess and Manilla Village than Fisherman’s Point (Table 3.13), and was significantly higher at the oyster shell and soft bottom habitats than the marsh edge habitat (Table 3.14). However, there was a significant site by habitat interaction ( $p < 0.002$ , Tables 3.13 and 3.15), which indicates that the main effects may not be independent. Total biomass was also significantly related to water temperature and salinity (Table 3.13), where total biomass generally increased as temperature and salinity increased (Figures 3.17 and 3.19 respectively). In addition, total biomass generally decreased as dissolved oxygen decreased (Figure 3.18), but not significantly.

Table 3.13. Analysis of variance of log (biomass + 1) of all fish species combined, among the three sites and habitats sampled. Biomass (g) based upon one hour gill net sets.

Log (biomass + 1)	d.f.	F	MS	p-value
Site	2	8.16	35.08	< 0.001
Habitat	2	21.06	90.56	< 0.001
Temperature	1	19.17	82.44	< 0.001
Salinity	1	5.69	24.48	< 0.01
Dissolved oxygen	1	0.98	4.22	< 0.32
Site x habitat	4	4.56	19.58	< 0.002

Table 3.14. Tukey HSD post-ANOVA test of log (biomass + 1) of all fish species combined, among the three sites and habitats sampled. Biomass (g) based on one hour gill net sets. Different letters indicate a significant difference.

Tukey HSD	Log (biomass + 1)	N	Site
A	6.1	70	Grand Terre/Queen Bess
A	6.1	71	Manilla Village
B	5.0	66	Fisherman's Point
B	4.5	68	Marsh edge
A	6.2	69	Soft bottom
A	6.6	70	Oyster shell

Table 3.15. Tukey HSD post-2 way ANOVA test of effects of log (biomass + 1) of all fish species combined comparing by site and habitat. Different letters indicate a significant difference.

SL	Marsh edge	Soft bottom	Oyster shell
Grand Terre/Queen Bess	6.46±0.54 ABC	6.92±0.52 AB	6.58±0.50 AB
Manilla Village	4.02±0.43 CD	6.71±0.44 AB	7.67±0.43 A
Fisherman's Point	2.83±0.52 D	5.04±0.52 BCD	5.50±0.52 ABC

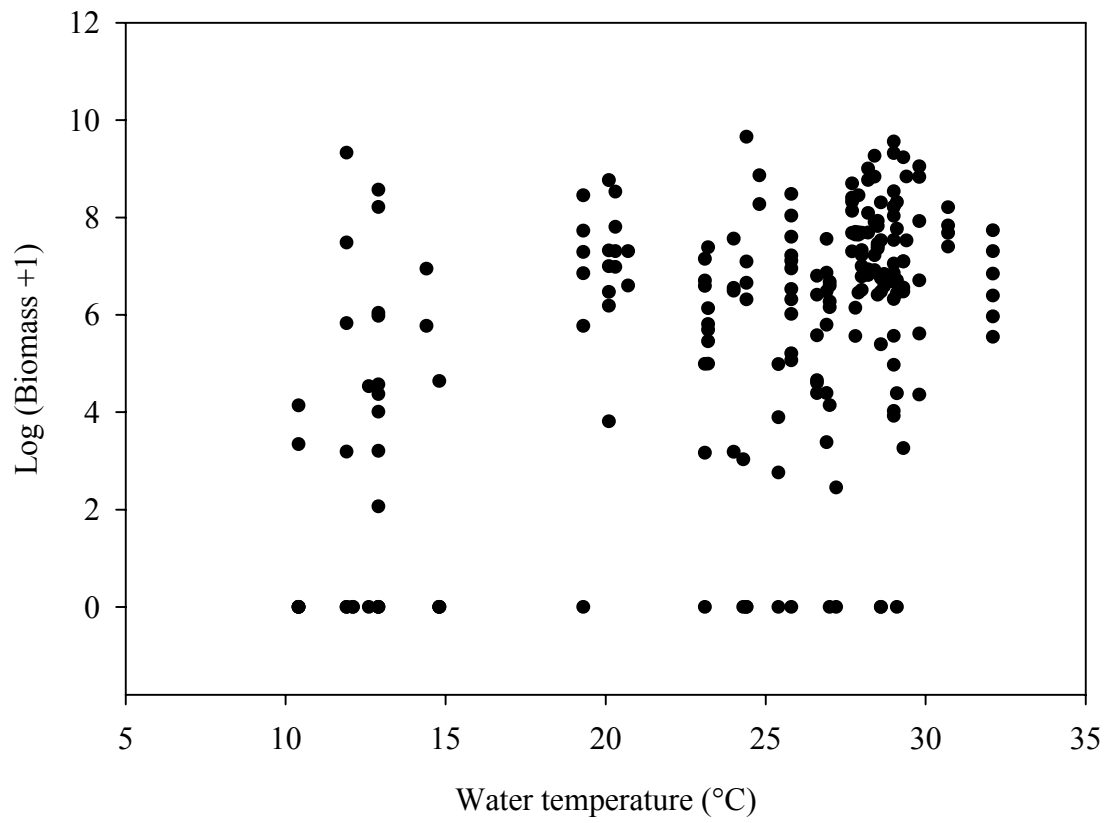


Figure 3.17. Relationship between biomass (g) and water temperature (°C) for all sites combined from May 2003 to May 2004.

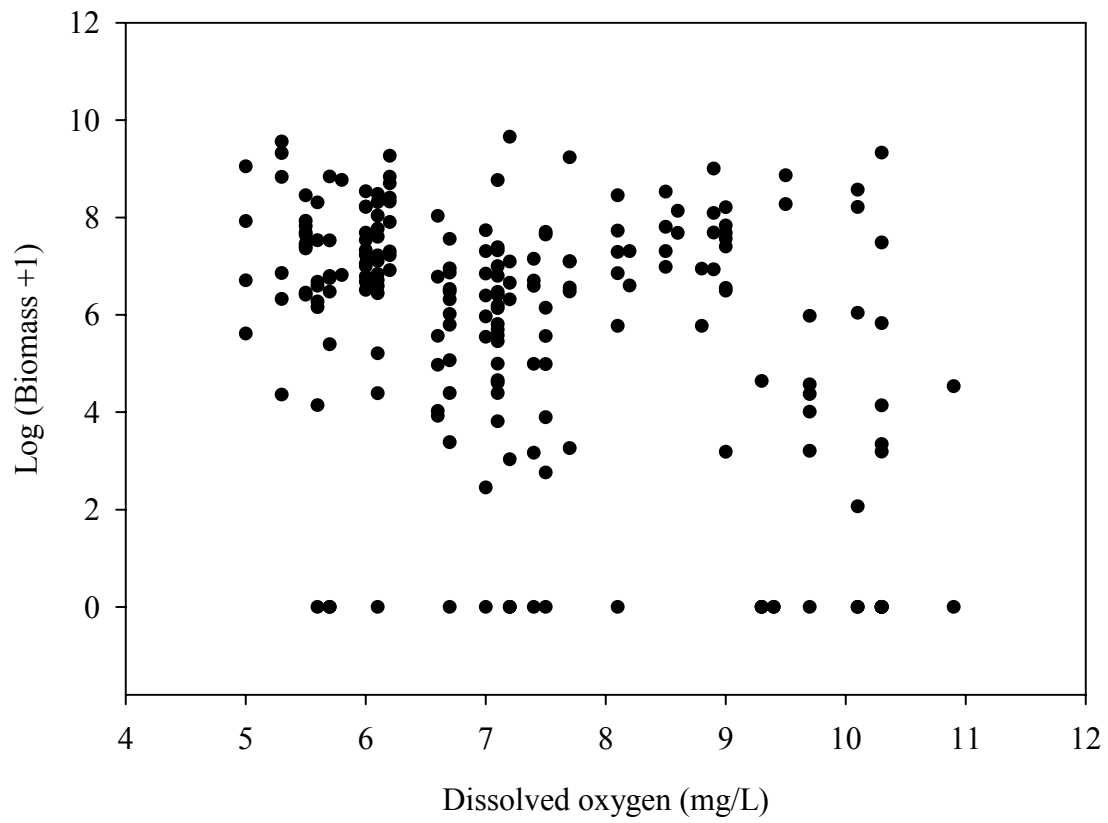


Figure 3.18. Relationship between biomass (g) and dissolved oxygen (mg/L) for all sites combined from May 2003 to May 2004.

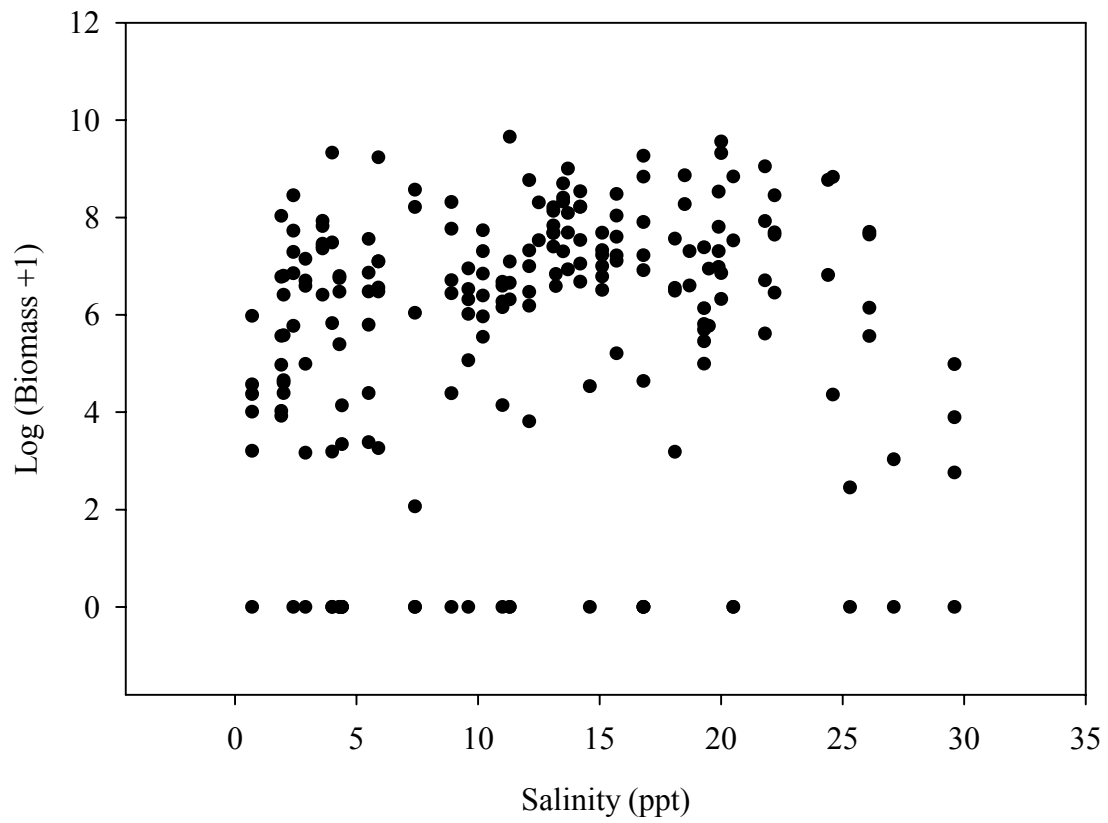


Figure 3.19. Relationship between biomass (g) and salinity (ppt) for all sites combined from May 2003 to May 2004.

### Summer Fish Assemblage Structure

Differences in fish assemblage structure were apparent among sites (Figure 3.20) from May to October 2003. The CA of the fish assemblage structure among sites explained 63% of the total variation on the first four axes (Table 3.13). The plot of sites contrasts the oligohaline site Fisherman's Point from the polyhaline site Grand Terre/Queen Bess, and the mesohaline site Manilla Village. This illustrates that the fish assemblage structure at Fisherman's Point was most dissimilar to the Grand Terre/Queen Bess and Manilla Village sites, while there was little difference in the fish assemblage structure among Grand Terre/Queen Bess and Manilla Village. The species driving these differences can be seen in Figure 3.21. The Atlantic needlefish (AN) was most common at Fisherman's Point, although it was found at least once at each of the other sites. The gizzard shad, *Dorosoma cepedianum* (GS), was most common at Fisherman's Point and Manilla Village, and was collected during only one sampling trip to Grand Terre/Queen Bess. The Atlantic croaker (AC), crevalle jack (CJ), Gulf menhaden (GM), sea catfish (SC), ladyfish (LF), red drum (RD), spotted seatrout (SPS), sand seatrout (SDS), spot (SP) and threadfin shad, *Dorosoma petenense* (TS) were found close to the origin (0,0) (Figure 3.21) indicating that they were all commonly collected at all three sites. The leather jacket (LJ), Atlantic threadfin herring (ATH), scaled sardine (SCS), Spanish mackerel (SPM), gafftopsail catfish (GF), silver perch (SLP), black drum (BD) and bighead searobin, *Prionotus tribulus* (BHS), were most common at Grand Terre/Queen Bess and Manilla Village and were rarely or never caught at Fisherman's Point. The pinfish (PF) and southern kingfish (SK) were most commonly found at Grand Terre/Queen Bess but were also rarely collected at Manilla Village, while the white mullet, *Mugil curema*, (WM) was found only at the Grand Terre/Queen Bess site. Thus, the Fisherman's Point site was distinguished from the other two sites by the presence

of the Atlantic needlefish, gizzard shad, and the lack of many species mentioned above that were commonly collected at Grand Terre/Queen Bess and Manilla Village.

Differences in fish assemblage structure were also apparent among habitats (Figure 3.22) from May to October 2003. The CA of the fish assemblage structure among habitats explained about 61% of the total variation on the first four axes (Table 3.13). The plot of habitats contrasts the marsh edge habitat from the soft bottom and oyster shell habitats, which illustrates that the fish assemblage structure differed along the marsh edge habitat as compared to the soft bottom and oyster shell habitats, while there was little difference in fish assemblage structure between the soft bottom and oyster shell habitats. The species driving these differences can be seen in Figure 3.23. The black drum, *Pogonias cromis*, (BD), striped mullet (SM) and white mullet (WM) were found only along the marsh edge and not at the soft bottom or oyster shell habitats. The gafftopsail catfish (GF), leather jacket (LJ), and red drum (RD) were found more often at the marsh edge habitat than soft bottom and oyster shell habitats, although they were found at least once at all habitat types. Species closest to the origin (0,0), Atlantic croaker (AC), Atlantic needlefish (AN), gizzard shad (GS), Gulf menhaden (GM), sea catfish (SC), ladyfish (LF), Spanish mackerel (SPM), spot (SP), spotted seatrout (SPS), and threadfin shad (TS), were commonly found at all habitat types. The southern kingfish (SK) and crevalle jack (CJ) are separated from the commonly found species along the first axis because they were most commonly collected at the soft bottom and oyster shell habitats, although they were each caught at least once along the marsh edge habitat. The bighead searobin (BHS) is clearly separated from the assemblage members associated with the marsh edge habitat along the first axis because it was collected only at the soft bottom and oyster shell habitats.

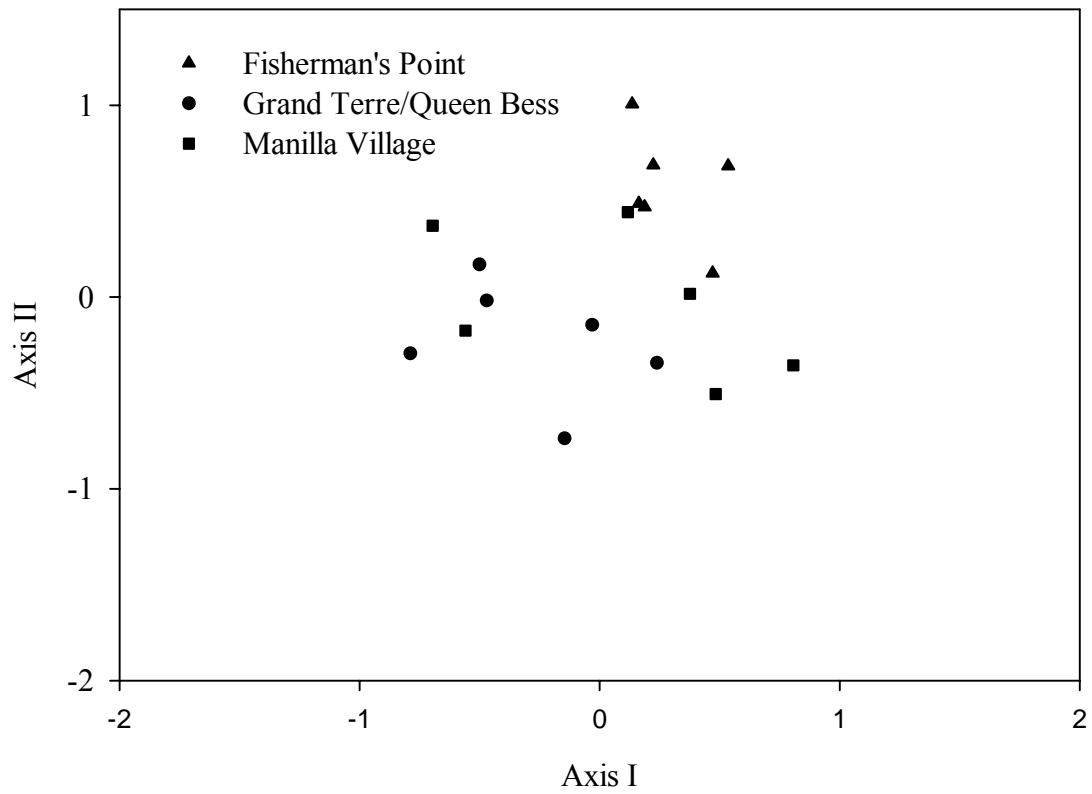


Figure 3.20. Association of sites based on a correspondence analysis of fish species presence/absence from May to October 2003. Individual symbols represent one month.

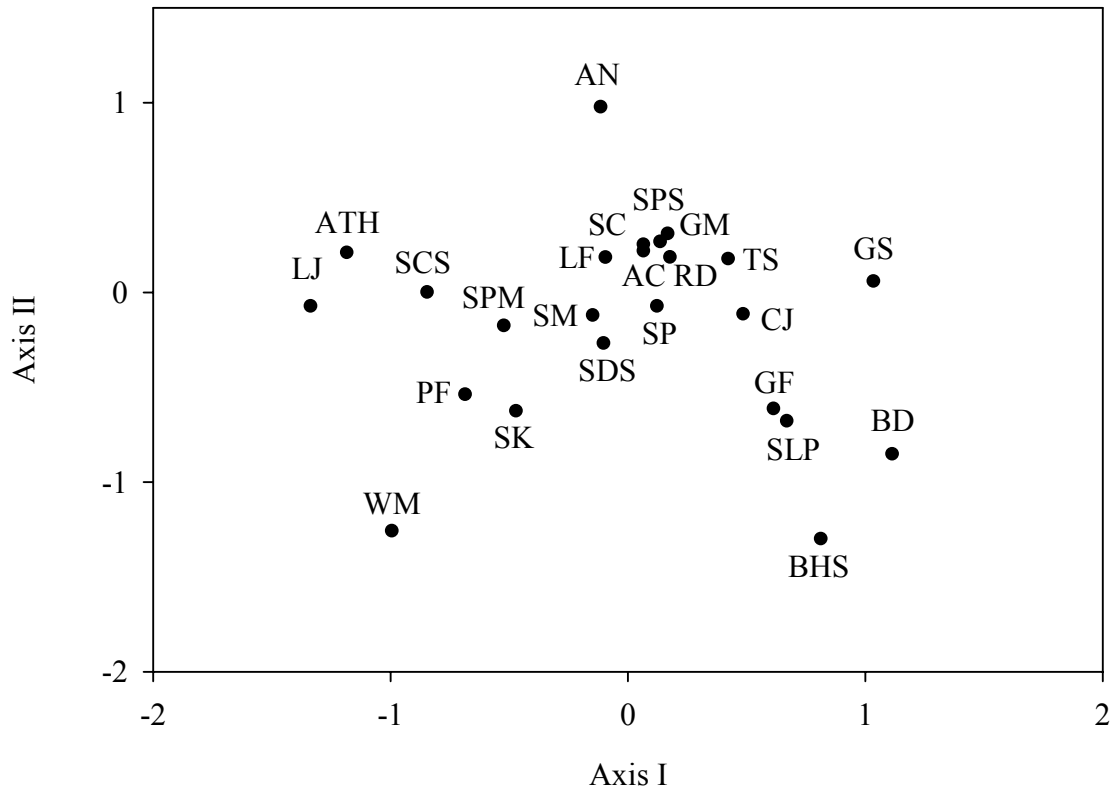


Figure 3.21. Association of fish species from a correspondence analysis of fish species presence/absence among sites from May to October 2003. Species codes are defined in Table 3.2.

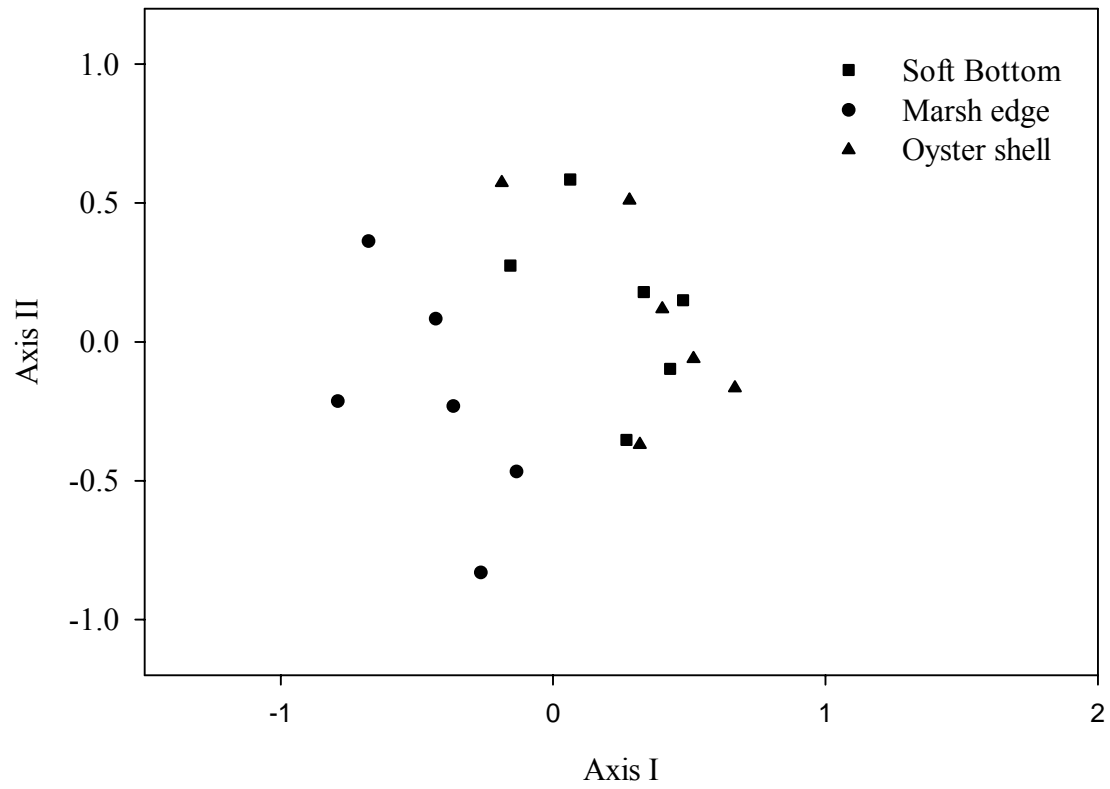


Figure 3.22. Association of habitats based on a correspondence analysis of fish species presence/absence from May to October 2003. Individual symbols represent one month.

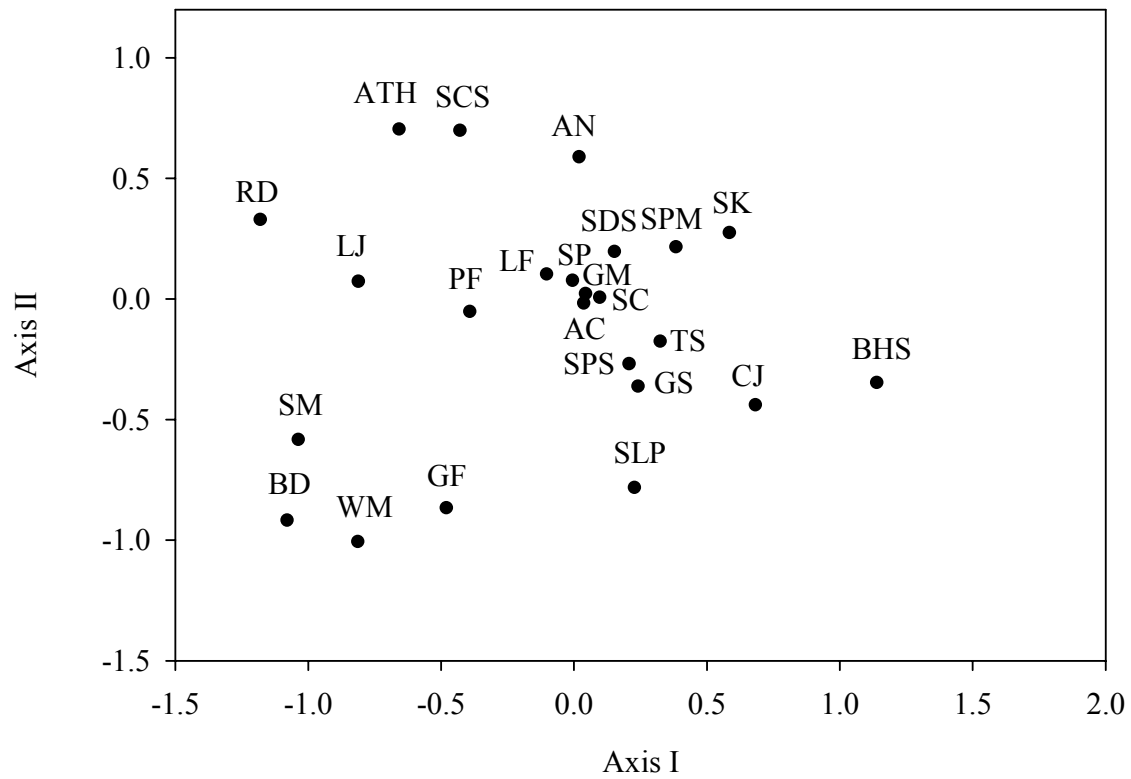


Figure 3.23. Association of fish species from a correspondence analysis of fish species presence/absence among habitats from May to October 2003. Species codes are defined in Table 3.2.

Table 3.16. Cumulative percentage of variance explained by the species site and habitat relationships based upon a correspondence analyses (corresponding to Figures 3.20 to 3.23).

Axes	1	2	3	4
Cumulative % variance by Site	23.12	40.81	54.77	62.98
Cumulative % variance by Habitat	20.93	36.65	50.03	61.26

### Annual Fish Assemblage Structure in Relation to Environmental Variables

The canonical correspondence analysis (CCA) indicates a strong relationship between fish assemblage structure and both habitat type and physical/chemical properties of the water (Figure 3.24). The first axis, which accounted for 34.5% of the variance, was best defined by salinity (Tables 3.14 and 3.15). Species such as leather jacket (LJ), scaled sardine (SCS) and white mullet (WM) were relatively more abundant in locations and/or at times when the salinity was relatively high, while the Atlantic needlefish (AN), gizzard shad (GS) and striped mullet (SM) were relatively more abundant in locations and/or at times when salinity was low.

The second axis, which accounted for 28.0% of the variation, was best defined by the marsh edge habitat (Tables 3.14 and 3.15). There is a clear distinction in the fish assemblage structure of the marsh edge habitat compared to both the soft bottom and oyster shell habitats. Species such as the leather jacket (LJ), red drum (RD), silver perch (SLP), striped mullet (SM) and white mullet (WM) were relatively more abundant along the marsh edge habitat. However, most species were found close to the origin, (e.g., Atlantic croaker (AC) and sea catfish (SC)), indicating that the relative abundance of these species was similar among habitats and ranges in the physical/chemical properties of the water.

The third axis accounted for about 22% of the variation. This variation was driven by temperature and dissolved oxygen. Given the two dimensional nature of the analysis it is difficult to go into any further detail as to how the fish assemblage was structured by these variables. However, in general the CCA offers an easily interpretable summary of species-environmental relationships along the first two axes and illustrates that salinity followed by differences in the marsh edge vs. soft bottom and oyster shell habitats were the most important environmental variables explaining fish assemblage structure, explaining 62.6% of the total variation (Table 3.14).

Table 3.17. Eigenvalues and cumulative percentage variance of species-environmental relationships based on a canonical correspondence analysis (corresponding to Figure 3.24).

Axes	1	2	3	4
Eigenvalues	0.153	0.125	0.097	0.052
Cumulative % variance of species-environmental relation	34.5	62.6	84.5	96.2

Table 3.18. Correlation coefficients for canonical correspondence analysis of fish assemblage structure in relation to environmental variables for the whole year.

Axes	1	2	2	4
Marsh edge	0.46	0.43	-0.28	0.01
Soft bottom	-0.29	-0.35	0.03	-0.15
Oyster shell	-0.13	-0.04	0.22	0.14
Dissolved oxygen	-0.08	0.22	0.40	0.31
Salinity	0.64	-0.35	0.03	-0.07
Temperature	0.03	-0.30	-0.53	0.16

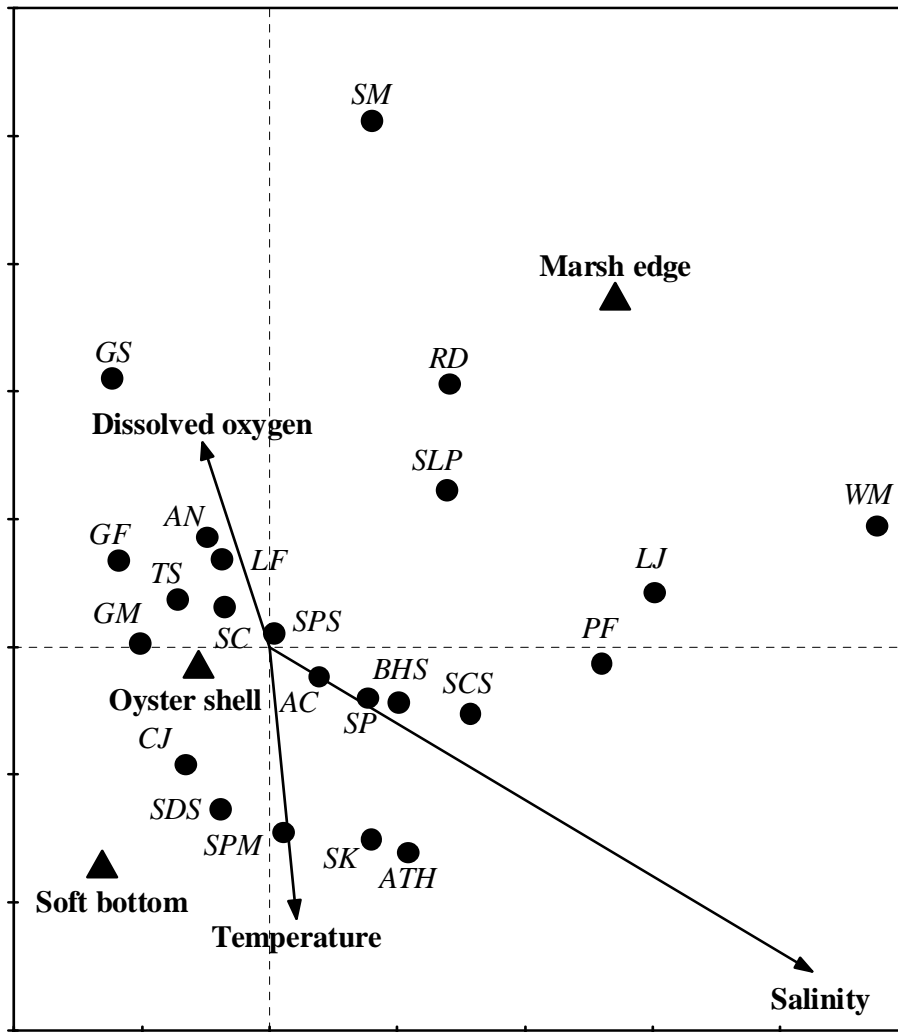


Figure 3.24. Association of fish species, habitats and physical/chemical water properties from a canonical correspondence analysis of fish abundance among sites from May 2003 to May 2004. Species codes defined in Table 3.2.

## Discussion

Physical/chemical properties of the water were important determinants of species richness, relative abundance and biomass in Barataria Bay, LA. In general, more fish were collected when the water temperature and salinity was highest and the dissolved oxygen was lowest. Thus, species richness, relative abundance and biomass were greatest during the warmer summer months and at the mid and lower bay sites, Manilla Village and Grand Terre/Queen Bess, where the salinity was relatively higher than at the upper bay site, Fisherman's Point. Plunket and LaPeyre (2005), who studied the fish assemblage structure in the mesohaline salinity range in Barataria Bay, LA, also found that catches of fish were highest in the warm summer months. The inverse relationship between species richness, relative abundance and biomass with dissolved oxygen is unlikely an indicator of the unimportance of dissolved oxygen to fish in this region, but rather, that fish were more abundant in the warm summer months when the DO was relatively low, as compared to the cool winter months when DO was the highest. At no time during this study did the DO reach below 5.0 mg/L, which is above lethal levels for most estuarine

Variability in fish behavior can cause large fluctuations in CPUE and hamper interpretations of CPUE data with respect to relative abundance (Hubert 1996). Moreover, gill nets have been shown to be influenced by numerous variables including water temperature, time of day, water level fluctuations, turbidity and currents (Hubert 1996). Gill nets are influenced by seasonal patterns in the movement and distribution of fish that occur as a result of spawning activity, habitat requirements and food availability (Hubert and O'Shea 1992). Gill nets are especially selective for species that move substantial distances in their daily routines (Hubert 1996). This study followed a precise sampling design that identified time of year, location,

duration and other habitat components of each sample, which has been suggested to reduce much of the variability when comparing CPUE over time and among locations (Hubert and O'Shea 1992; Mero and Willis 1992). None the less, it is possible that fish may not have been as active when the water temperature was lower in the winter months, thereby reducing their catchability in the gill net when the water temperature was lower.

A study in Louisiana by Felly (1987) found that fish assemblage structure differed between upper (fresh) and lower (estuarine) reaches of three tributaries to the Calcasieu estuary, LA, although the fresh water and estuarine reaches contained some species in common. This distribution of fish is not surprising given that small-bodied marsh residents are considered to have the broadest salinity tolerances and ranges of all estuarine fishes (Nordlie 2003). Jones et al. (2002) found that fish and macrobenthos assemblage structure differed in relation to temperature, DO, distance from shore, depth, substrate and salinity, in that order of importance. Contrary to this study, Peterson and Ross (1991) found a more diverse fish assemblage at the freshwater and oligohaline sites as compared to their mesohaline sites in Mississippi, although this difference between studies may be attributable to sampling with different gears (e.g., seine net vs. gill net).

In the present study, species richness, relative abundance and biomass were greater at the soft bottom and oyster shell habitats compared to the marsh edge habitat, although the presence of some species did differ among habitats. It is likely that small-bodied species commonly associated with marsh habitat were poorly sampled because the gill nets consisted of mesh sizes too large and because the gill net only sampled along the marsh edge and not on the marsh surface. Gill nets have also been shown to be size selective, biased against smaller fish, saturate and to be influenced by fish activity (Hubert 1996; Finstad and Berg 2004). A study by Birdsong (2005) sampled fish assemblage composition and relative abundance along the marsh edge by

seine nets in Barataria Bay, including Grand Terre, found a total of 59 species of which 32 species were not collected in the present study. The majority of these species were small-bodied species that are commonly found near or on the marsh (e.g. sailfin molly, *Poecilia latipinna*, and gulf killifish, *Fundulus grandis*), and are generally considered to be marsh residents (Deegan and Thompson 1985) and commonly found in marsh habitats throughout estuaries in the northern Gulf of Mexico (Minello and Rozas 2002).

It is also possible that cryptic and/or small species associated with soft bottom and oyster shell habitats were not vulnerable to the gear used in the present study. While gill nets were the most appropriate gear to use over habitats sampled, they are not without their biases as mentioned above. None the less, gill nets are easily deployed and used over oyster shell, which has been shown to be a habitat difficult to sample with many other gear types (Wenner et al. 1996). Moreover, gill nets met the objective of the study, which was to sample the sub-adult and adult species of recreational importance, and not to sample the marsh residents that use the marsh surface or the cryptic species that live within the nooks and crannies of the oyster shells.

The study by Plunket and LaPeyre (2005) found a total of 18 species by using gill nets and 10 species by using benthic sampling trays. Of those species collected with gill nets, 4 were absent during this study and included the striped blenny, *Chasmodes bosquianus*, crested blenny, *Hypleurochilus geminatus*, speckled worm eel, *Myrophis punctatus*, and a mangrove snapper, *Lutjanus griseus*. Those species collected with the benthic sampling trays included 10 species that were not collected during this study. The majority of these species were small-bodied, cryptic species e.g., the darter goby, *Gobionellus boleosoma*. The use of gill nets as a sampling gear may not have allowed collection of these species, because they are size selective gear where capture is a function of fish activity (Hubert 1996), and because they do not provide a substrate

for settlement or refuge like benthic trays. Although the gill nets used in this study, composed of a mesh ranging from 1.27 to 3.81 cm stretched mesh, are clearly size selective for some species they worked reasonably well for catching fish as small as striped anchovy, *Anchoa hepsetus*, (5.6 cm SL) and as large as a bull shark, *Carcharhinus leucas*, (81.3 cm SL).

The lack of difference in species richness, relative abundance and biomass among soft bottom and oyster shell habitats is supported by the investigation of Plunket and LaPeyre (2005), who also found no significant differences in the catch of fishes over soft bottom and oyster shell habitats when sampling with gill nets at a site near Manilla Village in Barataria Bay; however, their catches were generally higher at the oyster shell habitat. This finding contrasts with the literature, which suggests that oyster reef communities of fish and macro-invertebrates along the Atlantic and Gulf of Mexico coasts are highly diverse and include numerous species that are absent or found rarely in adjacent soft bottom habitats (see Coen et al. 1999). However, in this same study, Plunket and LaPeyre (2005) found that benthic tray catches of fish in Barataria Bay were greater over oyster shell habitats compared to soft bottom habitats. It is possible that the low relief production reefs, or cultch reefs, sampled during this study, that are seeded and harvested heavily each year may be functioning differently as fish habitat than natural oyster reefs, which are generally far more complex than those reefs sampled in this study.

Based upon my research, the fish assemblage structure in Barataria Bay can generally be divided into three categories, those fishes found only or mostly at the marsh edge (e.g., red drum, striped mullet), those species found at all three habitat types (e.g., Atlantic croaker and spot), and those few pelagic species which had a higher affinity for soft bottom and oyster shell habitats (e.g., Spanish mackerel, Gulf menhaden and sand seatrout). Despite the fact that richness, relative abundance and biomass were greater at the soft bottom and oyster shell habitats, the

marsh edge habitat had a distinct fish assemblage. Species such as the leatherjacket, red drum, striped mullet and white mullet were more often found along the marsh edge as compared to the soft bottom and oyster shell habitats. Moreover, few species were found to rely solely on oyster shell and/or soft bottom habitats.

By combining the fish assemblage data with the habitat and physical/chemical data over the whole sampling period (May 2003 to May 2004) with the CCA, salinity and habitat type appear to be the most important variables driving the variation in the Barataria Bay fish assemblage structure. It is important to keep in mind that this description of fish assemblage structure arranges species by their proportion in the catch in relation to environmental variables. Thus, although spotted seatrout are found near the centroid of the CCA and can be considered less influenced by salinity and temperature than the Atlantic threadfin herring, this observation does not mean that spotted seatrout were not affected by salinity and temperature. A closer look at spotted seatrout (see Chapter 1) indicates that spotted seatrout were more abundant when the salinity and water temperature were higher. However, the CCA does present a summary of fish assemblage structure and illustrates which fish species were commonly found together versus those that were rarely found at the same site. The CCA also indicates that the fish assemblage composition and relative abundance along the marsh edge was distinct from the soft bottom and oyster shell habitats, although many species were found at all three habitat types. Had different gears (e.g., seine net) been employed in this study, the distinction of this habitat would likely be even greater (Birdsong 2005; Plunket and LaPeyre 2005). Clearly the marsh edge habitat in Barataria Bay, LA, is of importance to many estuarine resident and transient species. This importance of the marsh edge habitat to estuarine dependant species in the northern Gulf of Mexico is supported by the literature, which has shown that marsh and marsh edge habitat act as

an important nursery and refugia habitat for many fish species (Boesch and Turner 1984; Minello 1999; Zimmerman et al. 2000; Minello and Rozas 2002).

Therefore the identification and description of essential fish habitat is a difficult task given the clear differences in species-specific habitat associations, the influence of physical/chemical properties of the water acting at both the species and assemblage level and the challenges with finding a gear that can collect all species present. This study illustrates the importance of moving fishery management in the direction of an ecosystem approach, given that relative habitat value is undoubtedly species-specific. However, it is clear that identifying and describing EFH on a species-specific level is a narrow approach given the interdependence of species and the complex biotic and abiotic interactions in an estuarine system such as Barataria Bay, LA. There is clearly a need to inventory multiple habitats with multiple gears to truly describe the fish assemblage structure in Barataria Bay, LA, before designating any habitat as essential. This task is currently underway here at Louisiana State University by a number of researchers, of which my project is just one portion of this greater study. None the less, based on my portion of this study, it appears that the marsh edge, soft bottom and oyster shell habitats likely serve as a mosaic of useable habitats as suggested by Bell et al. (1991) rather than as isolated units. Minello (1999) suggests that marsh edge, submerged aquatic vegetation, oyster reefs and shallow non-vegetated bottom are all likely essential for some fishery species. Moreover, it appears that the physical/chemical properties of the water work in concert with the different available habitats in structuring the fish assemblage in Barataria Bay. It is clear to me that the marsh plays a key role in sustaining fisheries in this region, given the affinity of most species to be associated with the marsh edge in some manner, although identifying it as essential is difficult based on the guidelines provided by NMFS. What I can say is that the marsh, oyster

shell and soft bottom habitats work in concert with the physical chemical properties of the water providing a heterogeneous ecosystem that supports a diverse fish community and that restoration should be on the ecosystem level for it to be most effective.

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## GENERAL SUMMARY AND CONCLUSIONS

The objectives of this study were to identify and describe essential fish habitat for recreationally important species in Barataria Bay, LA. Specifically, the focus of this study was to investigate the habitat preferences of spotted seatrout and variables affecting their distribution, relative abundance, biomass, length distribution and food web dynamics. This study went beyond a single species approach of identifying EFH by also investigating species composition, richness, relative abundance, and biomass of the whole fish assemblage among marsh edge, soft bottom and oyster shell habitats, and in relation to the physical/chemical properties of the water.

Chapter 1 indicates that habitat preferences of spotted seatrout are not easily defined by habitat type alone, but rather that their distribution, relative abundance, biomass and length distribution are more likely determined by a combination of habitat and physical/chemical properties of the water. The presence of spotted seatrout was driven by water temperature and a preference for the open water, while its relative abundance was best defined by temperature and salinity. There was little difference in the relative abundance of spotted seatrout among marsh edge, soft bottom and oyster shell habitats, although spotted seatrout were generally smaller at the marsh edge habitat. This trend suggests that the marsh edge habitat may be particularly important to juvenile spotted seatrout. Therefore it is difficult to define any of these habitats individually as essential for spotted seatrout. It is more likely that together these habitats make up an ecosystem that is essential for spotted seatrout. Thus, restoration efforts to restore the wetlands in coastal Louisiana will only help this species by maintaining the integrity of this important ecosystem, while efforts to build artificial oyster reefs may not have the anticipated benefits for spotted seatrout.

The results of Chapter 2 suggest that individual spotted seatrout may not move widely throughout Barataria Bay, rather they may exhibit some site fidelity with preference for salinity zones within the bay. This inference of regional habitat use is supported by the isotopic composition of the prey contents, which also reflected a similar pattern among sites along the oligohaline to polyhaline salinity gradient. Results also suggest that spotted seatrout exhibit some fidelity to habitat type whereby some individuals were spending more time at the marsh edge habitat as compared to soft bottom and oyster shell habitats. This study suggests that conclusions drawn about habitat use by spotted seatrout based solely on gut contents may not provide the full scope of relative habitat value within Barataria Bay, LA. Moreover, this study demonstrates that stable isotope analysis is a useful tool when investigating the food web dynamics of spotted seatrout in estuaries in the northern Gulf of Mexico.

Chapter 3 illustrates that the fish assemblage structure at Fisherman's Point was most dissimilar to the Grand Terre/Queen Bess and Manilla Village sites, while there was little difference in the fish assemblage structure among Grand Terre/Queen Bess and Manilla Village. Fisherman's Point site was distinguished from the other two sites by the presence of the Atlantic needlefish and gizzard shad, and the lack of many marine oriented species commonly collected at Grand Terre/Queen Bess and Manilla Village. Based on habitat, the fish assemblage structure in Barataria Bay could generally be divided into three categories, those only or mostly found at the marsh edge habitat (e.g., red drum, striped mullet), those species found at all three habitat types (e.g., Atlantic croaker and spot), and a few, mainly pelagic, species which had a higher affinity for soft bottom and oyster shell habitats (e.g., Spanish mackerel, Gulf menhaden and sand seatrout). It appears that these habitats and the physical/chemical properties of the water work in concert with one another to provide a diverse range of available habitats for estuarine

resident and transient species. Clearly our idea of what habitats are essential will differ greatly depending on which species is the focus of the study. Therefore, by taking an ecosystem approach to identifying essential fish habitat we ensure that one species is not protected at the expense of the others.

There is clearly a need to inventory multiple habitats with multiple gears to truly describe the fish assemblage structure in Baratraia Bay, LA, before designating any habitat as essential. This task is currently underway here at Louisiana State University by a number of researchers, myself included. The results from my portion of the study suggests that the available physical structure of marsh edge, soft bottom and oyster shell habitats work in concert with the physical/chemical properties of the water, providing a mosaic of useable habitats important to fishes in Barataria Bay. However, it appears that the marsh plays a key role in sustaining fisheries in this region, given the affinity of most species to be associated with the marsh edge in some manner, and the affinity of juvenile fishes for this habitat. Given that marsh loss is one of the greatest threats to the integrity of this estuarine ecosystem, I recommend that future research efforts focus on the restoration of this habitat.

Overall, this study illustrates that the identification and description of essential fish habitat is a difficult task given the clear differences in species-specific habitat associations, the influence of physical/chemical properties of the water acting at both the species and assemblage level and the challenges associated with finding a gear that can collect all species present. Moreover, I think identifying and describing essential fish habitat on a species-specific level is a narrow approach given the interdependence of fish species. I believe this study illustrates the importance of moving fisheries management in the direction of an ecosystem approach, given that relative habitat value is undoubtedly species-specific, and that this ecosystem has such a

diverse fish community. Whether or not we can identify any of the habitats investigated as essential is difficult based on the guidelines provided by NMFS. What I can say is that the marsh, oyster shell and soft bottom habitats work in concert with the physical chemical properties of the water providing a heterogeneous ecosystem that supports a diverse fish community and that restoration should be on the ecosystem level for it to be most effective. Therefore identifying essential fish habitat may not be a feasible approach to fishery conservation and management in coastal Louisiana because it may not be possible to identify which habitats are essential versus which ones are temporarily occupied.

APPENDIX 1. TOTAL CATCH OF SPECIES COLLECTED FROM GRAND TERRE/QUEEN BESS, MAY 2003 TO MAY 2004, PRESENTED BY FAMILY, SCIENTIFIC AND COMMON NAME AND SPECIES CODES USED IN FIGURES BY MONTH AND HABITAT TYPE. (A = ATLANTIC).

Family	Species	Common	ID	May-	May-
				03	03
				Marsh	Soft
Lepisosteidae	<i>Lepisosteus spatula</i>	Alligator gar	AG	0	0
Lepisosteidae	<i>Lepisosteus oculatus</i>	Spotted gar	SG	0	0
Clupeidae	<i>Dorosoma cepedianum</i>	Gizzard shad	GS	0	0
Clupeidae	<i>Dorosoma petenense</i>	Threadfin shad	TS	0	0
Clupeidae	<i>Alosa chrysochloris</i>	Skipjack herring	SJ	0	0
Sciaenidae	<i>Micropogonias undulatus</i>	A. croaker	AC	15	32
Sciaenidae	<i>Leiostomus xanthurus</i>	Spot	SP	52	107
Clupeidae	<i>Brevoortia patronus</i>	Gulf menhaden	GM	6	32
Sciaenidae	<i>Cynoscion arenarius</i>	Sand seatrout	SDS	2	6
Ariidae	<i>Arius felis</i>	Sea catfish	HC	3	0
Ariidae	<i>Bagre marinus</i>	Gafftopsail catfish	GF	0	0
Sparidae	<i>Archosargus probatocephalus</i>	Sheepshead	SH	0	0
Mugilidae	<i>Mugil cephalus</i>	Striped mullet	SM	1	0
Bothidae	<i>Citharichthys spilopterus</i>	Bay whiff	BW	0	0
Sciaenidae	<i>Bairdiella chrysoura</i>	Silver perch	SLP	92	0
Bothidae	<i>Paralichthys lethostigma</i>	Southern flounder	SF	0	0
Sydotidae	<i>Synodus foetens</i>	Inshore lizardfish	IL	0	0
Engraulidae	<i>Anchoa hepsetus</i>	Striped anchovy	STA	0	0
Triglidae	<i>Prionotus tribulus</i>	Bighead searobin	BHS	0	1
Trichiuridae	<i>Trichiurus lepturus</i>	A. cutlassfish	ACF	0	0
Carangidae	<i>Caranx hippos</i>	Crevalle jack	CJ	0	0
Sciaenidae	<i>Menticirrhus americanus</i>	Southern kingfish	SK	0	3
Sciaenidae	<i>Cynoscion nebulosus</i>	Spotted seatrout	SPS	5	1
Elopidae	<i>Elops saurus</i>	Ladyfish	LF	0	0
Clupeidae	<i>Opisthonema oglinum</i>	A. threadfin herring	ATH	0	0
Carangidae	<i>Trachinotus carolinus</i>	Florida pompano	FP	0	0
Sciaenidae	<i>Pogonias cromis</i>	Black drum	BD	0	0
Sciaenidae	<i>Sciaenops ocellatus</i>	Red drum	RD	0	0
Sparidae	<i>Lagodon rhomboides</i>	Pinfish	PF	0	1
Scombridae	<i>Scomberomorus maculatus</i>	Spanish mackerel	SPM	0	0
Clupeidae	<i>Harengula jaguana</i>	Scaled sardine	SCS	0	0
Belonidae	<i>Strongylura marina</i>	Atlantic needlefish	AN	0	0
Carangidae	<i>Oligoplites saurus</i>	Leather jacket	LJ	0	0
Rachyentridae	<i>Rachycentron canadum</i>	Cobia	CB	0	0
Mugilidae	<i>Mugil curema</i>	White mullet	WM	1	0
Carcharhinidae	<i>Carcharhinus leucas</i>	Bull shark	BS	0	0
Gerreidae	<i>Eucinostomus argenteus</i>	Spotfin mojarra	SF	0	0

APPENDIX 1 Cont'd.

	May-03	Jun-03	Jun-03	Jun-03	Jul-03	Jul-03	Jul-03	Aug-03	Aug-03	Aug-03
ID	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	0	0	1	0	0	0	0
TS	0	0	1	2	9	11	1	0	0	1
SJ	0	0	0	0	0	0	0	0	0	0
AC	8	2	0	4	1	0	3	5	0	5
SP	1	5	0	4	5	10	0	11	8	1
GM	8	11	29	31	58	545	15	0	6	39
SDS	0	0	0	4	0	1	0	0	8	1
HC	0	4	1	0	13	6	1	1	4	3
GC	0	0	0	0	1	0	0	0	0	0
SH	0	0	0	0	0	0	0	0	0	0
SM	0	2	0	0	1	0	0	1	0	0
BW	0	0	0	0	0	0	0	0	0	0
SLP	4	1	1	0	0	0	1	0	0	0
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	1	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	3	1	0	0	2	0
SK	0	0	0	2	12	4	1	0	3	2
SPS	9	4	3	2	10	0	2	6	16	2
LF	0	2	0	0	5	0	0	1	14	0
ATH	0	0	0	0	0	0	0	22	1	0
FP	0	0	0	0	0	0	0	0	0	0
BD	0	0	0	0	1	0	0	0	0	0
RD	0	1	0	0	0	0	0	1	0	0
PF	0	1	1	0	2	0	0	3	0	1
SPM	2	6	14	11	0	1	0	0	5	2
SCS	0	0	0	0	0	2	0	171	0	0
AN	0	0	0	0	0	0	0	0	0	0
LJ	0	0	0	0	0	0	0	11	0	1
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	0	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0

APPENDIX 1 Cont'd.

	Sep-03	Sep-03	Sep-03	Oct-03	Oct-03	Oct-03	Nov-03	Nov-03	Nov-03	Jan-04
ID	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Soft
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	0	0	0	0	0	0	0
TS	0	0	0	0	0	0	0	0	0	0
SJ	0	0	0	0	0	0	0	0	0	0
AC	6	1	10	3	0	0	1	1	0	0
SP	0	2	0	13	3	0	0	0	0	0
GM	20	194	26	0	0	0	0	0	0	0
SDS	0	33	2	2	0	0	0	0	0	0
HC	2	10	1	0	4	0	0	0	0	0
GC	0	0	0	0	0	0	0	0	0	0
SH	0	0	0	0	0	0	0	0	0	0
SM	0	0	0	0	0	0	0	0	0	0
BW	0	0	0	0	0	0	0	0	0	0
SLP	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	1	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	0	0	0	0	0
SK	0	3	2	0	0	1	0	1	1	0
SPS	0	8	0	0	0	0	0	0	0	0
LF	2	1	14	7	0	0	0	0	0	0
ATH	0	142	25	0	0	0	0	1	0	0
FP	0	0	0	0	0	0	0	0	0	0
BD	0	0	0	0	0	0	0	0	0	0
RD	1	0	0	0	0	0	0	0	0	0
PF	1	0	2	3	0	0	0	0	0	0
SPM	0	3	7	0	1	0	0	0	0	0
SCS	8	78	0	0	0	0	0	0	0	0
AN	2	0	0	3	0	0	0	0	0	0
LJ	0	0	0	3	0	0	1	0	0	0
CB	0	1	0	0	0	0	0	0	0	0
WM	0	0	0	1	0	0	2	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	1	0	0	0	0	0	0	0	0

APPENDIX 1 Cont'd.

ID	Jan-	Feb-	Feb-	Feb-	Mar-	Mar-	Mar-	Apr-	Apr-	Apr-
	04	04	04	04	04	04	04	04	04	04
	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	0	0	0	0	0	0	0
TS	0	0	0	0	0	0	0	0	0	0
SJ	1	0	1	0	0	0	0	0	0	0
AC	0	0	0	0	0	0	0	4	45	6
SP	0	0	0	2	0	1	0	0	12	1
GM	0	0	0	0	0	45	2	0	4	0
SDS	0	0	0	0	0	1	1	0	0	0
HC	0	0	0	0	5	3	1	0	2	6
GC	0	0	0	0	0	0	0	0	1	1
SH	0	0	0	0	0	0	0	0	0	0
SM	0	0	0	0	1	0	0	0	0	0
BW	0	0	0	0	0	0	0	0	0	0
SLP	0	0	0	32	46	0	3	0	6	1
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	0	0	0	0	0
SK	0	0	0	0	0	0	2	1	5	0
SPS	0	0	0	0	0	0	0	1	0	2
LF	0	0	0	0	0	0	0	0	0	0
ATH	0	0	0	0	0	0	0	0	0	0
FP	0	0	0	0	0	0	0	0	1	0
BD	0	0	0	0	0	0	0	0	0	0
RD	0	0	0	0	0	0	0	0	0	0
PF	0	0	0	0	0	0	0	0	0	0
SPM	0	0	0	0	0	1	1	0	0	8
SCS	0	0	0	0	0	0	0	0	0	0
AN	0	0	0	0	0	0	0	0	0	0
LJ	0	0	0	0	0	0	0	0	0	0
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	0	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0

## APPENDIX 1 Cont'd.

	May- 04	May- 04	May- 04
ID	Marsh	Soft	Oyster
AG	0	0	0
SG	0	0	0
GS	0	0	0
TS	2	3	1
SJ	0	0	0
AC	3	53	5
SP	16	147	1
GM	15	108	38
SDS	0	18	1
HC	1	1	1
GC	0	0	0
SH	0	0	0
SM	4	0	1
BW	0	0	0
SLP	6	0	0
SF	0	0	0
IL	0	0	0
STA	0	0	0
BHS	4	1	0
ACF	0	0	0
CJ	0	0	0
SK	0	13	1
SPS	4	10	5
LF	0	0	0
ATH	0	0	0
FP	0	0	0
BD	0	0	0
RD	0	0	0
PF	0	0	0
SPM	0	0	1
SCS	0	0	0
AN	0	0	0
LJ	0	0	0
CB	0	0	0
WM	0	0	0
BS	0	0	0
SF	0	0	0

APPENDIX 2. TOTAL CATCH OF SPECIES COLLECTED FROM MANILLA VILLAGE,  
MAY 2003 TO MAY 2004, PRESENTED BY FAMILY, SCIENTIFIC AND COMMON  
NAME AND SPECIES CODES USED IN FIGURES BY MONTH  
AND HABITAT TYPE. (A = ATLANTIC).

Family	Species	Common	ID	May-	May-
				03 Marsh	03 Soft
Lepisosteidae	<i>Lepisosteus spatula</i>	Alligator gar	AG	0	0
Lepisosteidae	<i>Lepisosteus oculatus</i>	Spotted gar	SG	0	0
Clupeidae	<i>Dorosoma cepedianum</i>	Gizzard shad	GS	0	0
Clupeidae	<i>Dorosoma petenense</i>	Threadfin shad	TS	1	0
Clupeidae	<i>Alosa chrysochloris</i>	Skipjack herring	SJ	0	0
Sciaenidae	<i>Micropogonias undulatus</i>	A. croaker	AC	1	4
Sciaenidae	<i>Leiostomus xanthurus</i>	Spot	SP	0	0
Clupeidae	<i>Brevoortia patronus</i>	Gulf menhaden	GM	87	81
Sciaenidae	<i>Cynoscion arenarius</i>	Sand seatrout	SDS	1	2
Ariidae	<i>Arius felis</i>	Sea catfish	HC	5	0
Ariidae	<i>Bagre marinus</i>	Gafftopsail catfish	GC	2	0
Sparidae	<i>Archosargus probatocephalus</i>	Sheepshead	SH	0	0
Mugilidae	<i>Mugil cephalus</i>	Striped mullet	SM	0	0
Bothidae	<i>Citharichthys spilopterus</i>	Bay whiff	BW	0	0
Sciaenidae	<i>Bairdiella chrysoura</i>	Silver perch	SLP	0	0
Bothidae	<i>Paralichthys lethostigma</i>	Southern flounder	SF	0	0
Sydotidae	<i>Synodus foetens</i>	Inshore lizardfish	IL	0	0
Engraulidae	<i>Anchoa hepsetus</i>	Striped anchovy	STA	0	0
Triglidae	<i>Prionotus tribulus</i>	Bighead searobin	BHS	0	0
Trichiuridae	<i>Trichiurus lepturus</i>	A. cutlassfish	ACF	0	0
Carangidae	<i>Caranx hippos</i>	Crevalle jack	CJ	0	0
Sciaenidae	<i>Menticirrhus americanus</i>	Southern kingfish	SK	0	0
Sciaenidae	<i>Cynoscion nebulosus</i>	Spotted seatrout	SPS	2	0
Elopidae	<i>Elops saurus</i>	Ladyfish	LF	0	0
Clupeidae	<i>Opisthonema oglinum</i>	A. threadfin herring	ATH	0	0
Carangidae	<i>Trachinotus carolinus</i>	Florida pompano	FP	0	0
Sciaenidae	<i>Pogonias cromis</i>	Black drum	BD	0	0
Sciaenidae	<i>Sciaenops ocellatus</i>	Red drum	RD	0	0
Sparidae	<i>Lagodon rhomboides</i>	Pinfish	PF	0	0
Scombridae	<i>Scomberomorus maculatus</i>	Spanish mackerel	SPM	0	0
Clupeidae	<i>Harengula jaguana</i>	Scaled sardine	SCS	0	0
Belonidae	<i>Strongylura marina</i>	Atlantic needlefish	AN	0	0
Carangidae	<i>Oligoplites saurus</i>	Leather jacket	LJ	0	0
Rachyentridae	<i>Rachycentron canadum</i>	Cobia	CB	0	0
Mugilidae	<i>Mugil curema</i>	White mullet	WM	0	0
Carcharhinidae	<i>Carcharhinus leucas</i>	Bull shark	BS	0	0
Gerreidae	<i>Eucinostomus argenteus</i>	Spotfin mojarra	SF	0	0

APPENDIX 2 Cont'd.

	May-03	Jun-03	Jun-03	Jun-03	Jul-03	Jul-03	Jul-03	Aug-03	Aug-03	Aug-03
ID	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	0	2	1	0	0	1	1
TS	0	0	3	0	2	0	2	0	5	5
SJ	1	0	0	0	0	0	0	0	0	0
AC	10	1	1	1	1	0	5	3	1	3
SP	3	0	0	0	1	0	0	1	11	6
GM	426	0	91	775	9	187	18	0	20	5
SDS	4	0	0	0	0	6	9	0	8	10
HC	3	0	0	8	1	2	31	3	0	4
GC	0	0	0	0	0	0	0	1	0	2
SH	0	0	0	0	0	0	0	0	0	0
SM	0	0	0	0	1	0	0	0	0	0
BW	0	0	0	0	0	0	0	1	0	0
SLP	3	0	0	0	0	1	2	1	0	2
SF	0	0	0	0	0	0	0	0	1	1
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	1	0	0	0	0
BHS	1	0	0	0	0	0	0	0	0	2
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	0	1	0	5	1
SK	1	0	0	0	0	0	0	0	0	0
SPS	15	0	3	4	0	3	2	1	10	3
LF	0	0	0	0	4	2	5	3	0	1
ATH	0	0	0	0	0	0	0	0	0	0
FP	0	0	0	0	0	0	0	0	0	0
BD	0	0	0	0	0	0	0	1	0	0
RD	0	0	0	0	0	0	0	1	0	0
PF	0	0	0	0	0	0	0	0	0	0
SPM	0	1	3	2	0	2	1	0	0	0
SCS	0	0	0	0	0	0	0	0	0	0
AN	0	0	0	0	0	0	0	0	0	0
LJ	0	0	0	0	0	0	0	0	0	0
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	0	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0

APPENDIX 2 Cont'd.

ID	Sep-03	Sep-03	Sep-03	Oct-03	Oct-03	Oct-03	Nov-03	Nov-03	Nov-03	Jan-04
	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	0	0	0	0	0	0	0
TS	0	0	0	2	0	1	0	0	0	0
SJ	0	0	0	0	0	0	0	0	0	0
AC	6	0	2	4	0	7	0	1	0	0
SP	0	0	0	1	9	24	3	1	0	0
GM	2	67	55	3	56	261	1	4	14	0
SDS	1	0	0	0	2	1	0	2	0	0
HC	4	5	3	5	0	5	0	3	0	0
GC	0	0	0	0	1	0	0	0	0	0
SH	0	0	0	0	0	0	0	0	0	1
SM	1	0	0	1	0	0	0	0	0	0
BW	0	0	0	0	0	0	0	0	0	0
SLP	0	0	0	0	0	0	1	0	3	0
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	0	0	0	0	0
SK	0	0	0	0	1	2	0	0	0	0
SPS	1	1	0	0	0	0	3	0	0	0
LF	4	2	1	1	0	0	0	0	0	0
ATH	6	22	37	1	0	0	0	0	0	0
FP	0	0	0	0	0	0	0	0	0	0
BD	0	0	0	0	0	0	0	0	0	0
RD	0	0	0	0	0	0	0	0	0	0
PF	0	0	0	0	1	0	1	0	1	0
SPM	0	6	4	1	1	1	0	0	0	0
SCS	5	8	2	6	4	5	0	0	0	0
AN	0	0	1	0	0	0	0	0	1	0
LJ	1	0	0	11	4	0	0	0	15	0
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	2	0	2	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	1	0	0	0	0

APPENDIX 2 Cont'd.

ID	Jan-04	Jan-04	Feb-04	Feb-04	Feb-04	Mar-04	Mar-04	Mar-04	Apr-04	Apr-04
	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	0	0	1	0	0	0	0
TS	1	0	0	0	0	0	1	1	0	0
SJ	0	1	0	0	1	0	0	0	0	0
AC	0	0	0	0	0	0	0	0	0	0
SP	0	0	0	0	2	0	0	0	0	1
GM	1	1	0	3	12	0	28	37	0	22
SDS	0	0	0	0	0	0	0	0	0	1
HC	0	0	0	0	0	0	2	2	0	2
GC	0	0	0	0	0	0	0	0	0	1
SH	0	0	1	0	1	0	0	0	0	0
SM	0	0	0	0	0	1	0	0	0	0
BW	0	0	0	0	0	0	0	0	0	0
SLP	0	0	0	0	1	1	1	81	0	0
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	0	0	0	0	0
SK	0	0	0	0	0	0	0	0	0	0
SPS	0	5	0	0	1	0	1	3	0	3
LF	0	0	0	0	0	0	0	0	0	0
ATH	0	0	0	0	0	0	0	0	0	0
FP	0	0	0	0	0	0	0	0	0	0
BD	1	1	0	1	4	0	0	1	0	0
RD	0	0	0	0	0	0	0	0	0	0
PF	0	0	0	0	0	0	0	0	0	0
SPM	0	0	0	0	0	0	0	0	0	0
SCS	0	0	0	0	0	0	0	0	0	0
AN	0	0	0	0	0	0	0	0	0	0
LJ	0	0	0	0	0	0	0	0	0	0
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	0	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0

APPENDIX 2 Cont'd.

ID	Apr-04 Oyster	May-04 Marsh	May-04 Soft	May-04 Oyster
AG	0	0	0	0
SG	0	0	0	0
GS	0	0	0	0
TS	0	0	0	0
SJ	0	0	1	1
AC	2	1	0	6
SP	0	1	1	3
GM	32	0	7	116
SDS	0	0	3	2
HC	7	0	0	3
GC	1	0	3	4
SH	0	0	0	0
SM	0	0	0	0
BW	0	0	0	0
SLP	3	0	0	3
SF	0	0	0	0
IL	0	0	0	0
STA	0	0	0	0
BHS	0	0	0	0
ACF	0	0	0	0
CJ	0	0	0	0
SK	1	0	0	1
SPS	6	0	2	2
LF	0	0	0	0
ATH	1	0	0	0
FP	0	0	0	0
BD	0	0	0	0
RD	0	0	0	0
PF	0	0	0	0
SPM	0	0	0	0
SCS	0	0	0	0
AN	0	0	0	0
LJ	0	0	0	0
CB	0	0	0	0
WM	0	0	0	0
BS	1	0	0	0
SF	0	0	0	0

APPENDIX 3. TOTAL CATCH OF SPECIES COLLECTED FROM FISHERMAN'S POINT,  
MAY 2003 TO MAY 2004, PRESENTED BY FAMILY, SCIENTIFIC AND COMMON  
NAME AND SPECIES CODES USED IN FIGURES BY MONTH  
AND HABITAT TYPE. (A = ATLANTIC).

Family	Species	Common	ID	May-	May-
				03 Marsh	03 Soft
Lepisosteidae	<i>Lepisosteus spatula</i>	Alligator gar	AG	0	0
Lepisosteidae	<i>Lepisosteus oculatus</i>	Spotted gar	SG	0	0
Clupeidae	<i>Dorosoma cepedianum</i>	Gizzard shad	GS	0	0
Clupeidae	<i>Dorosoma petenense</i>	Threadfin shad	TS	0	0
Clupeidae	<i>Alosa chrysochloris</i>	Skipjack herring	SJ	0	0
Sciaenidae	<i>Micropogonias undulatus</i>	A. croaker	AC	1	0
Sciaenidae	<i>Leiostomus xanthurus</i>	Spot	SP	0	0
Clupeidae	<i>Brevoortia patronus</i>	Gulf menhaden	GM	2	33
Sciaenidae	<i>Cynoscion arenarius</i>	Sand seatrout	SDS	0	0
Ariidae	<i>Arius felis</i>	Sea catfish	HC	0	0
Ariidae	<i>Bagre marinus</i>	Gafftopsail catfish	GC	0	0
Sparidae	<i>Archosargus probatocephalus</i>	Sheepshead	SH	0	0
Mugilidae	<i>Mugil cephalus</i>	Striped mullet	SM	0	0
Bothidae	<i>Citharichthys spilopterus</i>	Bay whiff	BW	0	0
Sciaenidae	<i>Bairdiella chrysoura</i>	Silver perch	SLP	0	0
Bothidae	<i>Paralichthys lethostigma</i>	Southern flounder	SF	0	0
Sydotidae	<i>Synodus foetens</i>	Inshore lizardfish	IL	0	0
Engraulidae	<i>Anchoa hepsetus</i>	Striped anchovy	STA	0	0
Triglidae	<i>Prionotus tribulus</i>	Bighead searobin	BHS	0	0
Trichiuridae	<i>Trichiurus lepturus</i>	A. cutlassfish	ACF	0	0
Carangidae	<i>Caranx hippos</i>	Crevalle jack	CJ	0	0
Sciaenidae	<i>Menticirrhus americanus</i>	Southern kingfish	SK	0	0
Sciaenidae	<i>Cynoscion nebulosus</i>	Spotted seatrout	SPS	0	0
Elopidae	<i>Elops saurus</i>	Ladyfish	LF	0	0
Clupeidae	<i>Opisthonema oglinum</i>	A. threadfin herring	ATH	0	0
Carangidae	<i>Trachinotus carolinus</i>	Florida pompano	FP	0	0
Sciaenidae	<i>Pogonias cromis</i>	Black drum	BD	0	0
Sciaenidae	<i>Sciaenops ocellatus</i>	Red drum	RD	0	0
Sparidae	<i>Lagodon rhomboides</i>	Pinfish	PF	0	0
Scombridae	<i>Scomberomorus maculatus</i>	Spanish mackerel	SPM	0	0
Clupeidae	<i>Harengula jaguana</i>	Scaled sardine	SCS	0	0
Belonidae	<i>Strongylura marina</i>	Atlantic needlefish	AN	0	1
Carangidae	<i>Oligoplites saurus</i>	Leather jacket	LJ	0	0
Rachyentridae	<i>Rachycentron canadum</i>	Cobia	CB	0	0
Mugilidae	<i>Mugil curema</i>	White mullet	WM	0	0
Carcharhinidae	<i>Carcharhinus leucas</i>	Bull shark	BS	0	0
Gerreidae	<i>Eucinostomus argenteus</i>	Spotfin mojarra	SF	0	0

APPENDIX 3 Cont'd.

ID	May-	Jun-	Jun-	Jun-	Jul-	Jul-	Jul-	Aug-	Aug-	Aug-
	03	03	03	03	03	03	03	03	03	03
	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	0	0	0	0	0	1	0
TS	0	0	0	0	0	1	0	0	0	1
SJ	0	0	0	0	0	0	0	0	0	0
AC	1	0	2	2	0	0	4	1	1	5
SP	0	0	0	2	0	0	0	0	0	4
GM	34	0	14	12	0	10	1	6	63	72
SDS	0	0	0	0	0	0	1	1	2	4
HC	2	0	2	2	0	0	4	10	1	12
GC	0	0	0	0	0	0	0	0	0	2
SH	0	0	0	0	0	0	0	0	0	0
SM	0	0	0	0	3	0	0	1	0	0
BW	0	0	0	0	0	0	0	1	0	0
SLP	0	0	0	0	0	0	0	2	0	3
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	1	0	0	0	0
SK	0	0	0	0	0	0	0	0	0	0
SPS	2	0	2	1	0	0	1	0	0	0
LF	0	0	0	2	4	0	24	2	6	22
ATH	0	0	0	0	0	0	0	0	0	0
FP	0	0	0	0	0	0	0	0	0	0
BD	0	0	0	0	0	0	0	0	0	0
RD	0	0	0	0	0	0	0	1	0	0
PF	0	0	0	0	0	0	0	0	0	0
SPM	0	0	0	0	0	0	0	0	0	0
SCS	0	0	0	0	0	0	0	0	0	0
AN	0	0	0	0	1	0	1	0	1	0
LJ	0	0	0	0	0	0	0	0	0	0
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	0	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0

APPENDIX 3 Cont'd.

ID	Sep-03	Sep-03	Sep-03	Oct-03	Oct-03	Oct-03	Jan-04	Jan-04	Jan-04	Feb-04
	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh
AG	0	0	0	0	0	0	0	0	0	0
SG	0	0	0	0	0	0	0	0	0	0
GS	0	0	0	1	0	0	0	0	1	0
TS	0	0	1	0	0	4	0	0	0	0
SJ	0	0	0	0	0	0	0	0	0	0
AC	1	2	4	0	1	2	0	0	0	0
SP	1	1	2	0	1	4	0	0	0	0
GM	0	13	3	0	58	35	0	3	0	0
SDS	0	0	0	0	0	0	0	0	0	0
HC	0	6	2	0	1	1	0	0	0	0
GC	0	0	0	0	0	0	0	0	0	0
SH	0	0	0	0	0	0	0	0	0	0
SM	0	0	0	0	0	0	0	0	0	2
BW	0	0	0	0	0	0	0	0	0	0
SLP	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	0	0	0	0	0
SK	0	0	0	0	0	0	0	0	0	0
SPS	4	0	0	0	0	0	0	0	0	0
LF	1	1	1	0	0	0	0	0	0	0
ATH	0	0	0	0	0	0	0	0	0	0
FP	0	0	0	0	0	0	0	0	0	0
BD	0	0	0	0	0	0	0	0	0	0
RD	2	0	1	0	0	0	0	0	0	0
PF	0	0	0	0	0	0	0	0	0	0
SPM	0	0	0	0	0	0	0	0	0	0
SCS	0	0	0	0	0	0	0	0	0	0
AN	0	2	2	1	1	1	0	0	0	0
LJ	0	0	0	0	0	0	0	0	0	0
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	0	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	1	0	0	0	0	0	0

APPENDIX 3 Cont'd.

ID	Feb-04	Feb-04	Mar-04	Mar-04	Mar-04	Apr-04	Apr-04	Apr-04	May-04	May-04
	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft	Oyster	Marsh	Soft
AG	0	0	0	0	1	0	0	0	0	0
SG	0	0	0	1	0	0	0	0	0	0
GS	0	0	0	0	1	0	0	0	0	0
TS	0	0	0	1	2	0	0	0	0	0
SJ	0	0	0	2	1	0	0	1	1	2
AC	0	0	0	1	0	0	1	0	0	1
SP	0	1	0	0	0	0	0	0	0	0
GM	5	0	0	100	136	1	37	44	0	6
SDS	0	0	0	0	0	0	0	0	0	0
HC	0	0	0	2	6	0	0	1	0	2
GC	0	0	0	0	0	0	0	0	0	1
SH	0	0	0	0	0	0	0	0	0	0
SM	0	0	1	0	0	0	0	0	1	0
BW	0	0	0	0	0	0	0	0	0	0
SLP	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0
IL	0	0	0	0	0	0	0	0	0	0
STA	0	0	0	0	0	0	0	0	0	0
BHS	0	0	0	0	0	0	0	0	0	0
ACF	0	0	0	0	0	0	0	0	0	0
CJ	0	0	0	0	0	0	0	0	0	0
SK	0	0	0	0	0	0	0	0	0	0
SPS	0	1	0	0	1	1	0	0	0	1
LF	0	0	0	0	0	0	0	0	0	0
ATH	0	0	0	0	0	0	0	0	0	0
FP	0	0	0	0	0	0	0	0	0	0
BD	0	0	0	0	0	0	0	1	0	0
RD	0	0	0	0	0	0	0	0	0	0
PF	0	0	0	0	0	0	0	0	0	0
SPM	0	0	0	0	0	0	0	0	0	0
SCS	0	0	0	0	0	0	0	0	0	0
AN	0	0	0	1	0	0	0	0	1	0
LJ	0	0	0	0	0	0	0	0	0	0
CB	0	0	0	0	0	0	0	0	0	0
WM	0	0	0	0	0	0	0	0	0	0
BS	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0

APPENDIX 3 Cont'd.

ID	May-04 Oyster
AG	0
SG	0
GS	0
TS	0
SJ	0
AC	3
SP	0
GM	2
SDS	0
HC	3
GC	2
SH	0
SM	2
BW	0
SLP	0
SF	0
IL	0
STA	0
BHS	0
ACF	0
CJ	0
SK	0
SPS	1
LF	0
ATH	0
FP	0
BD	0
RD	0
PF	0
SPM	0
SCS	0
AN	0
LJ	0
CB	0
WM	0
BS	0
SF	0

## VITA

Pamela S. D. MacRae was born on October 16, 1974, in Halifax, Nova Scotia, Canada. She is the daughter of Gayle Ellesbeth MacRae and Wayne Carlton MacRae and the sister of Andrea Georgina Charlotte MacRae. Pam was graduated from Sackville High School in 1993. She received a Bachelor of Science degree and Honors Certificate in biology from Saint Mary's University, Halifax, Nova Scotia, in 1996 and 1997 respectively. She then moved to Toronto, Ontario, and received a Master of Science degree in zoology with the Aquatic Ecology Group at the University of Toronto in 1999. Pam worked as a fishery technician for the Toronto Conservation Authority in 1999 and then as a fishery biologist for the Lake Simcoe Fisheries Assessment Unit, Ontario Ministry of Natural Resources, until the summer of 2001. In the fall of 2001, she became a graduate research assistant under Dr. James H. Cowan Jr. in the Coastal Fisheries Institute, Department of Oceanography and Coastal Sciences at Louisiana State University. Pam will receive a Doctor of Philosophy degree from the Department of Oceanography and Coastal Sciences in August of 2006.